Hase San both Sides

protein search, using frame\_plus\_n2p model OM nucleic -

September 10, 2004, 14:19:44 ; Search time 68.5 Seconds (without alignments) 7473.450 Million cell updates/sec Run on:

US-10-039-272-1 4850 Title: Perfect score: Sequence:

Scoring table:

0.5 7.0 7.0 BLOSUM62 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext 283366 segs, 96191526 residues Searched:

566732 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Approx MMD avector	Dael 17 protein	moral to proceed a	meralloma-associate	meranocyce-specifi	hidronia antigen n	rector true-ric	procein-tyrosine-p	aportpoprocern(a)	Gurfage seets:	ANA PROFESSION CY	Athragonian D	himothetical and	histidine rich alv	The recommendation of the second seco
	4	TD	138065	853871	T38400	A41234	A49179	T07907	A41105	T18518	S21766	\$50820	T02831	155976	T15840	KGHUGH	
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	4	match Length DB	560	626	662	668	491	446	926	2869	555	2395	1541	457	2946	525	
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## ALIGNMENTS

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gene NMB protein - human

C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #text\_change 05-Nov-1999
C;Accession: 138065
C;Accession: 138065
R;Weterman, M.A.; Ajubi, N.; van Dinter, I.M.; Degen, W.G.; van Muijen, G.N.; Ruitter, I Int. J. Cancer 60, 73-81, 1995
A;Title: nmb, a novel gene, is expressed in low-metastatic human melanoma cell lines an.
A;Reference numb, a novel gene, is expressed in low-metastatic human melanoma cell lines an.

A; Accession: I38065

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-560 <RES>
A;Cross-references: EMBL:X76534; NID:g666042; PIDN:CAA54044.1; PID:g666043

A; Gene: GDB: NMB C;Genetics:

A; Cross-references: GDB:120237; OMIM:162340 A;Map position: 15g22-15gter

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 9.6e-252 2999.00 99.82% 99.82% 61.84% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.:

5559

US-10-039-272-1 (1-2661) x I38065 (1-560)

120 GCCGCCAAACGATTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAG 179 21 AlaAlaLysArgPheHisAspValLeuGlyAsnGluArgProSerAlaTyrMetArgGlu 40 ð Q D

GTCGTGACCTGCCAAGGGAGCATTCCCACGGAGGTCTGTACCATCATTTCTGACCCCACC 1318 CACACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCA 1018 GGACCTIGICCGCCACCGCCACCACCACCAGACCTICAAAACCCACCCTTCTTTAGGA 1078 1198 1258 380 400 779 240 838 260 898 280 300 719 220 359 100 419 120 479 140 539 160 599 180 629 200 299 9 80 CCTGCTGGTGACAACCCCCTGGAGCTGAGTAGGATTCCTGATGAAAACTGCCAGATTAAC AGATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATC ATCCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAAGCTCCCTAATAGACTTT GlyGlnTyrPheGlnLysLeuGlyArgCysSerValArgValSerValAsnThrAlaAsn ATTATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCCAATTATTCTACCATTAAC ACTATIGITCCAGAAGGAACGATCGAAATTCATCCGACGAAACCTTGCC-AAAGATCTCCCC CCTTTTCCTCACCACCCCGGATGGAAGATGGAATTTCATCTACGTCTTCCACACTT GTGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATAT GTTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTG AGAAATGAGGCTGGTTTATCTGGTGATCCATATGTTTACAACTGGACAGCATGGTCAGAG GACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAA CACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAACTCTACCCA GTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTG ATATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGC GGTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAAT 180

1738 1438 1498 1558 1618 1678 540 560 520 480 500 440 460 TTCCCGGGAAACCAGGAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCT TGCGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTG GIGATCICCCTCTIGGIGIACAAAAACACAAGGAATACAACCAATAGAAATAGICT GGGAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAAGCCGTGTTC ACTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCCTGGGGGAT GACACAAGCCTGGCTCTCACGAGCACCTGATTTCTGTTCCTGACAGAGACCCAGCCTCG CCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACT 1679 441 1559 1619 1379 1439 461 1499 481 1319 421 401 RESULT S53871 g 8 ò 원 ò g ò Dp g à Db ð ð ò

Description of the protein of the pr PID:9887941 GB:U14133; NID:9887940; PIDN:AAA69538.1; A;Residues: 1-626 <KWO>A;Cross-references: GB:

626 184 97 207 191 22 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.49e-46 635.00 41.45% 27.14% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

(1-626)US-10-039-272-1 (1-2661) x S53871

251 311 131 53 72 40 28 ||||||| ||||||---ThrLysThrTrpAsnArgGlnLeuTyrProGluTrpThr---GGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGT AATGGCTGGTCTTCTGATGAAATGAATGAAAAAAACTCTACCCAGTGTGGAAGCGG TICCIGGGATTICIGCTCCTGCCTGCAAGATTGCCACTTGATGCC AsnGlnAspTrpLeuGlyValProArgGlnLeuVal--78 σ 192 29 g q ò g à qq à à

Meise Sun py 7, 2,9 Page

Db 23	Qy 23	Qy 24	Qy 24	Qy 25-	Qy 26(	RESULT 5 HSNMB LOCUS	DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS TITLE JOURNAL	FEATURES		gene	}			
		140	146			164		1707 TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTCGACCTTGTTTCTGAAGCTCA 1766 		1827 ATTATTGTAAATAGATATTGTGGTAAGTTGAAGTTGAATTTTTATAGGTTAAATGTCA 1886 	1887 ITTTAGAGATGGGGGGGGGTTATACTGCAGGGAGCTTCAGCCATGTTGTGAAACTGAT 1946 	1947 AAAAGCAACTTAGCAAGGCTTCTTTCATTATTTTTTTTAGCTTATAAAGTCTTAG 2006 	2007 GTAACTAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAAGCTACTATTGATTA 2066 	2067 GAGCCTAACCCAGGTTAACTGCAAGAAGGGGGGGATACTTTCAGCTTTCCATGTAACTG 2126	21	2187 CTTCAATACACACTCATGAACTCCTGATGGAACAATAACAGGCCCAAGCCTGTGGTATGA 2246 	2247 TGTGCACACTTGCTACACTCAGAAAAATACTACTCTCATAAATGGGTGGG	2307 GTGACAACCTACTTGCTTGGCTGAAGGAATGATATTCATATTTATT
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340 GIGACAACCTACTITGCTIGGCTGAGTGAAGGAATGAIATTCAIAIACATTTAITCA 2399 460 TATTICCAAAITTITGTATAGTCGCTGCACATAITTGAAATC-ATATATAAGACTTTCC 2518 PRI 09-FEB-1995 /proteIn id="CAA5404.1"

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Direct Submission
Submitted (03-DEC-1993) M. Weterman, University of Nijmegen, of Biochemistry, PO Box 9101, 6500 HB Nijmegen, NETHERLANDS
Location/Qualifiers mRNA 607 -AAAATGAGGGAAGACACAAAAAAAAAAA 2636 /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" 2669 bp /clone="MNB" /clone="MNI" /clone lib="MVI" 1. 269 /gene="NMB" /gene="NMB" /codon\_start=1 Homo sapiens (human) H.sapiens NMB mRNA. X76534 X76534.1 GI:666042 NMB gene. 427 367 487

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2006 2039 2066 1946 1706 1739 1766 1886 1919 1559 1586 1619 1646 1679 1826 1859 1526 1466 1499 1079 1106 1139 1199 1226 1259 1286 1319 1346 1379 1406 1439 TITTAGAGATGGGGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT GTAACTAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGC 1680 GIGTCTTTCTCAACCGIGCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGC TACTCAAAAACCAAGAATTTAAAAGAGTTTCTTAAATTTCGACCTTGTTTCTGAAGCTCA TGATTTCTGTTCCTGACAGAGCCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCTGA GCCCTGTGGATGTGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG TGCCATGGCCTCAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCA CCAGACCTTCAAAACCCCACCCTTCTTAAGACCTGCTGGTGACAACCCCCTGGAGGTGA CAATTGTAGAGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGG CCAGACCTTCAAAACCCACCCTTCTTTAGGACCTGCTGGTGGTAGAACCCCCTGGAGGTGA

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Contact: MGC help desk

Bmail: cgapbs-r@mail.nh.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Dy: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc mgc@nhgri.nih.gov/

Contact: nisc mgc@nhgri.nih.gov/

Contact: nisc mgc@nhgri.nih.gov/

Contact: N. Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Massiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M. A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Scries: IRAK Plate: 68 Row: k Collumn: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505404.
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Anote="Mptor" Region: Repeats in polycystic kidney disease 1 (PKD1) and other proteins"

Ab_xref="CDD:smart00089"
                                                                                                                                                                                       Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Proc. Natl. Acad. Sci.
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TITLE
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buecrow, K.H., Schaefer, C.F., Bhat, N.K.,
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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GAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCCATGTAACTG
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                                                     2100 GAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCCATGTAACTG
                                                                                                             2127 IAIGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA
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Run on:

Sequence:

Minimum DB Maximum DB

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homo sapien
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mus musculu
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                                                                                                                   homo sapien
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TISSUE-Peripheral blood;

MEDLINE-2498106; PubMed=12609765;

Bandari P.S., Qian J., Yehla G., Joshi D.D., Maloof P.B., Potian J., Oh H.S., Gascon P., Harrison J.S., Rameshwar P.;

"Hematopoietic growth factor inducible neurokinin-1 type: a transmembrane protein that is similar to neurokinin 1 interacts with substance P.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Melanoma;
MEDLINE=95113576; PubMed=7814155;
MEDLINE=95113576; PubMed=7814155;
MEDLINE=95113576; PubMed=7814155;
Van Muijen G.N.P., Ruiter D.J., Bloemers H.P.J.;
"NMB, a novel gene, is expressed in low-metastatic human melanoma cell lines and xenografts.";
Int. J. Cancer 60:73-81 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Regul. Pept. (11:169-178(2003).

-: FUNCTION: Could be a melanogenic enzyme (By similarity).

-: SUBCELLULAR LOCATION: Type I membrane protein (Potential).

-: TISSUE SPECIFICITY: Not restricted to the melanocytic lineage.

-: DEVELOPMENTAL STAGE: Expression in poorly metastatic melanoma ilnes; no expression in highly metastatic melanoma coll similarity: BELONGS TO THE PMEL-17/NMB FAMILY.

-: SIMILARITY: Contains 1 PXD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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P22670
Q05858
P35658
Q86t65 ]
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Putative transmembrane protein NMB precursor (Transmembrane
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GPBA_HUMAN
RB_MOUSE
                                           RB MOUSE
YE68 METJA
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AT10_MOUSE
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AR41 SCHPO
PER1 VOLCA
ENV FENV1
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RFX1_HUMAN
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P3K2_DICDI
CYSP_SCHMA
REP_ECOLI
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MOUSE
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SAH1 HUMAN
HED1 HUMAN
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GPNMB OR NMB OR HGFIN.
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NCBI_TaxID=9606;
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-MODEL=frame+_n2p.model -DEV=xlp

-MODEL=frame+_n2p.model -DEV=xlp

-MODEL=frame+_n2p.model -DEV=xlp

-G=/cgn2_1/USPPO. Spool | JVSD10393277/runat_07092004_144222_21619/app_query.fasta_1.2823

-DB=SwissProt_42-QFNT=fastan_SUFFIERS - MINARTCH=0.1 -LGOPCL=0 -LGOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LISF=45

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LISF=45

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LISF=45

-UNITS=bits -START=1 -END=-1 -MATRIX=Bord=0 -THR MIN-0 -ALIGN=15 -MODE=LOCAL

-UNITS=bits -START=1 -END=-1 -MATRIX=Bord=10 -NAXIEN=10 -NAXIEN=10 -LONGLOG

-UNITS=bits -START=1 -END=-1 -MATRIX=Bord=1 -NGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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090372 coturnix co
060696 mus musculu
098917 gallus gall
P40967 homo sapien
006154 hose taurus
P29074 homo sapien
060519 mus musculu
P04196 homo sapien
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                                                                                                                                                                                                                                                    Description
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                              Compugen Ltd.
                                                                                protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                                       141681 seqs, 52070155 residues
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GACACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCG
          CCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGGTTGGCCATATTTGTCACT
                                            GTGATCTCCCTTTGGTGTACAAAAACACAAAGGAATACAACCCAATAGAAAATAGTCCT
                                                                             TICCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAAGGAGTTTCT
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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Turque N., Denhez F., Martin P., Planque N., Bailly M., Begue
Stehelin D., Saule S.;
                                                                                                                                                                                                                                                                                                                                          "Characterization of a new melanocyte-specific gene (QNR-71) expressed in v-myc-transformed quail neuroretina."; EMBO J. 15:3338-3350(1996).
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15-MAR-2004 (Rel. 43, Last annotation update)
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SMART; SM00089; PKD; 1.
PROSITE; PS50093; PKD; 1.
Signal; Transmembrane; Glycoprotein.
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|187 GlyArgSerSerAlaAsnPheSerValAsnThrAlaAsnIleThrLeuGlyLysHisIle
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                                                    NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                    Disease mutation.
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                                                                                                                                                                                                                                                      HisAspproSerTyrTyrLeuAsnAspSerAlalleSerTyrLysTrpAsnPheGlyAsp
                                                                                                                                   980 ACCTICAGCCTIAACCICACIGIGAAAGCIGCAGCACCAGGACCITGICCGCCACCCCA
                                                                                                                                             345 AspProSerAlaProAsnGluMetAlaGluAspAsn---ProAspGlyGlyCysHisIle
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ThrThrTyrValValThrAspLysIleProlleLeuValSerMetSerGlnLysHisAsp
                                       920 AATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / -> SSASLRSSRPRPW (IN SILVER).
                                                                                                                                                                                                                       Signal; Melanin biosynthesis; Repeat;
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7 X 13 AA APPROXIMATE TANDEM REPEATS.
                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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15-MAR-2004 (Rel. 43, Last annotation update)
Melanocyte protein Pmel 17 precursor (Silver locus protein)
SILV OR PMEL17 OR DIOH12S53E OR SI.
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MELANOCYTE PROTEIN PMEL 17.
EXTRACELLULAR (POTENTIAL).
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RKQPAPOWTAGLIILKAPWISWG (;
7AB94ID2E3FB1044 CRC64;
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S -> L (IN SILVER)
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STRAIN=C57BL/6; TISSUE=Skin;
MEDLINE=95175358; PubMed=7870580;
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PIR, SS3871; SS3871.
MGD; MGI:98301; Si.
InterProx; IPRO00601; PKD.
Pfam; PF00801; PKD; 1.
SMART; SM00089; PKD; 1.
PROSITE; PS50003; PKD; 1.
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Best Local Similarity:
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Qy         1012		395 ThrThrValAlaGlnAlaThrThrThrGluGlyProAspAlaSerProLeuLeuPro 413 1100GAGCTGAGTAGGATTCCTGATGAA	1124	A54 LeuAspilevalGinGlyileGluSerAlaGluIleLeuGln 467  Qy 1223 CCGGTGCCATGACTCCCTAATAGACTTTGTCGTGACCGCAAGGGAGCATT 1282	1283 CCCACGGAGGTCTGTACCATTTCTGACCCCACCTGCGAGATCACCCAGAACACAGTC		DD 548 SerThrGlnLeuValValProGlyGlnAspGlyGlyLeuGlyGln 562  QY 1520 GCCTGATCTCCGTTGGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTG 1573	QY 1574 GTGTACAAAAACACAAGGAATACAACCCAATAGAA 1609 ::: Db ::: 583 LeuGlyIleAspLeuArgSerArgAlaGlnPheProLysCysHisMetValAlaLeuThr 602	1610	OY 1670 GCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAA 1723	RESULT 4
Query Match:         13.09*         Indels:         191           DB:         1         Gaps:         22           US-10-039-272-1         (1-2661) x PM17_MOUSE (1-626)         (1-626)           QY         78 TTCCTGGGATTTCTGCTCCTGGCGAAGATTGCCACTTGATGCCGCCAAACGA 131           Db         9 PheLeuProvalLeuValLeuSerAlaLeuLeuAlaValG1yAlaLeuG1uG1ySerArg 28           QY         132 TTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGGCACAATCAAT	2 AATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAACTCTACCCAGTGTGGAAGCGG 1ThrLysThrTpAshargGlacuTyrProGlutrpThr 2 GGAGACATGAAGAAAAACTCTACGAAAAACTCTACCCAGTGTGGAAGCGGG	312 GACTCACCAGCCTCGTCGTGTGCTGTGCTGTGCTGTGCT	372 TGCCAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAACTGCAGAAATGAG 428	113 SerdinvaltrøglyglyglidprovåltyrproGlidjuproaspasp 128 489 GGGBAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCT 548 129 Ala	CACCACCCGGAIGGAGAAGAIGGAATITCAICTACGTCTTCCACACACATGGTCAGIAI	### SACTICAACTICATGAAGTGATGTCTACAGAAGACATGGACGGGCATATGT 	200 LeuAlaHisAlaSerSerThrPheThrIleThrAspGlnValPrOPheSerValSerVal 219 786 TTCCAGAA	AATTATTCT ::: AlaGluAla		950 ACTGTGAATCACAGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCT 1009 	1010 GCA 1012 

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AATCACACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCA 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCA-------GGACCTTGTCCGCCACCCACCACCAGACCTTCAAAACCC 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 ProbeuSerSerCysdlyThrSerAlaProProValValAspPro---ThrThrGlyPro 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 AlaTrpGlyLysArgGlyArgPheValTyrValTrpTrpThrTrpGlyArgTyrTrpGln 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 GCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAG 380
                                                                                                                                                                                                                                                                                                                                                     100 ValLeuProAspGlyArgValValTrpSerGlnAsnCysThrValAsnGlyThrArgMet 119
                                                                                                                                                                                                                                                                                                                                                                                          TTATCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAA 494
                                                                                                                                                                                                                                                                                                                                                                                                                   120 LeuglnGlyAspPro---ValTyrPro---GluGlnLeuAlaGluGlySerAspGly--- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                              495 AAIGGCACCGGCCAAAAGCCAICAIAACGICTICCCTGAIGGGAAACCITITCCICACCAC 554
                                                               CIGCTCCIGGCIGCAAGAIIGCCACTIGAIGCCGCCAAACGAITICAIGAIGIGCIGGGC 149
                                                                                                                                                                                                                                                                                                         80 ThrLeuValGlyAlaArgAlaThrPheSerileAlaLeuArgPheProGlyThrGlnThr 99
                                                                                                                                          20 GlnGlnArgGlyGlyGlyArgSerArgGlyGlyValLysGlySerAlaTrpGlyGlyArg 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                               675 CAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGG---GCATATGTTCCCATCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 TyrThrMetGluValValValTyrHisTyrArgGlyArgGlnArgPheIleProlleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 732 CAAGIGAAAGAIGIGIACGIGGIAACAGAICAGATICCIGIGITIGIGACIAIGITCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           615 AAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGGCCT
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                                                                                                                                                                                                                                                                                                                                      381 GAAGATGCCAATGGCAACATAGTCTATGAGAACTGC-----AGAAATGAGGCTGGT
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                                                                                                                  ---TCTGATGAAAATGACTGGAATGAAAACTCTACCCAGTGTGGAAGCGGGGAGACATG
                                                                                                                                                                                                 40 ProAlaProPheArgSerirpAspThrAlaArgTyrArgProTrpGlnGludiyThrAla
                                                                                                                                                                                                                            261 AGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCA
                                                                                                                                                                                                                                             228 LeuGluValAlaAlaGlyAspGlyGlySerPheValArgAsnArg
269
                                        US-10-039-272-1 (1-2661) x P115_CHICK (1-762)
                                                                                             ValLeuLeuAlaAlaLeuLeuAlaLeu-
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                                                                                                                                                                                                                                                                                       X 20-24 AA APPROXIMATE TANDEM REPEATS
                                                                      Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                        PREMELANOSOME.
--- TISSUE SPECIFICITY: Specific to pigmented epithelial cells and melanocytes. Not expressed in lens, neural retina, brain, heart, gizzard or liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: Expressed during the redifferentiation of pigmented epithelial cells (PEC).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                       STRAIN=White leghorn; TISSUB=Retinal pigment epithelium; MEDLINE=92020667; PubMed=1924173; Mochii M., Agata K., Eguchi G.; "Complete sequence and expression of a cDNA encoding a chicken
                                                                                                                                                                                                                                                                STRAIN=White leghorn; TISSUE=Retinal pigment epithelium; MEDLINE=88311098; PubMed=3409326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .LINKED (GLCNAC. . .) (PA 172C8DDB4FDCE7C6 CRC64;
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171
80
186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PTM: Glycosylated.
-!- SIMILARITY: BELONGS TO THE PMEL-17/NMB FAMILY.
-!- SIMILARITY: Contains 1 PKD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
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N-LINKED (GLCNAC.
                      15-WAR-2004 (Rel. 43, Last annotation update)
115 kDa melanosomal matrix protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
           (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                            115-kDa melanosomal matrix protein.";
Pigment Cell Res. 4:41-47(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77356 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat.
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35.60%
24.26%
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Pfam; PR0801; PKD.
SWART; SM00089; PKD; 1.
PROSITE; PS50093; PKD; 1.
Signal; Glycoprotein; Repeat
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                                                                Gallus gallus (Chicken)
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Best Local Similarity:
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659
762 J
                                                                                                                     NCBI_TaxID=9031;
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4465
489
509
1111
1115
346
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            15-JUL-1998
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REPEAT
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CARBOHYD
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-!- SIMII
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us-10-039-272-1.rsp

1996   1997   1998   1997   1998	Qý Dp		Db d0	:::  SerileP
342 ThrAlaDroSechanleuthrdlySercilyThrAlaAlaAlaProGlyThrThrAla   161	⋩		RESULT 5	
1996   1997   1996   1997   1998   1999	q	ThralaProSerAsnLeuThrGlySerGlyThrAlaAlaAlaProGlyThrThrAlaAla	5	AN 27.51.5
362   ProductyladercityAladrochrotyvalServalAladriewiserksp 381   DEE   1097 - CTOSACCTOAGTAGATTCTCTART	λζ			995 (1
1937CYGANGCTGAGATTCCTGAT-   1120	q	ProArgAlaSerGlyAlaProAlaGluProThrGlyValSerValAlaValLeuSerAsp		400
382   SerWedGulthGulteGulProAspProValleuSerThrAlaValAlaAspAlaAla 401	<i></i> ₹	CTGGAGCTGAGTAGGATTCCTGAT		3P100)
1120     112	ð	:::    SerMetGluThrGluProLeuProAspProValLeuSerThrAlaValAlaAspAlaAla		MEL17
402 AladiyThrAspProThtAlaAspProGeuProThrSerValSerSerGlyGlyAsp 421   RP     1120	δy			a; Met
1120	ą	AlaGlyThrAspProThrAlaAspProLeuProProThrSerValSerSerGlyGlyAsp		D=96(
422   AlabrodlyThrValAlablaDroThrAlaValGluGlySerValAlaAlaGlyValGlyThr	λį			FROM N.
1120	Q	AlaProGlyThrValAlaProThrAlaValGluGlySerValAlaAlaGlyValGlyThr		Chi
442 AlaGluAspValAlaAlaAlaAlaThrProGlyAlaThrAlaAlaAspValAlaAlaAspThr 461	λį			
### 462 AladlyAlaThrAspGlyAspAlaValGlyPrOThrAlaAlaThrAlaGluSerIIe 491 ### 1120 ### 1	Db	AlaGluAspValAlaAlaAlaThrProGlyAlaThrAlaAlaAspValAlaValAspThr		mouse
462 AladiyAlaThirkspdlyAspAlaValGiyProThrAlaAlaAlaThirAlaGluSerile 481  1120	δy			1. A
1120	QQ	AlaGlyAlaThrAspGlyAspAlaValGlyProThrAlaAlaAlaThrAlaGluSerIle		FROM 43275
482 AlaAspProThrAlaGlyAlaThrAspGlyAspAlaValGlyAlaThrAlaGluSerIle 501  1120	ζ			r, de
1120	д	AlaAspProThrAlaGlyAlaThrAspGlyAspAlaValGlyAlaThrAlaGluSerIle		p100.
S02	ΟŻ			
1120	Ф	AlaAspProThrAlaGlyAlaThrAspGlyAspAlaValGlyProThrAlaAlaAlaThr		61540
120	>-			organ.
1120	٥	AlaGluSerIleAlaAspProThrAlaGlyAlaThrAlaValSerSerGlySerAlaThr		. Der
542 AlaGlyAlaThrAlaGluProLeuLeuValLySArgGlnAlaProGluAlaGluPro 561 RA 1121 GAAACTGCCAGATTACAGATATCGCCACTTTCAAGCCACTCACATTGTAGAGGA 1180 S62 ThrGlyCySValLeuTyzArgTyrGlyThrPhelei::	>-			FROM
1121 GARAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCACAATTGTAGGGGA 1180	0	AlaGlyAlaThrAlaGluProLeuLeuLeuValLysArgGlnAlaProGluAlaGluPro		4.351 A., M
	_	GAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACAATCACAATTGTAGAAACAAAAAAAA		and e
1181 ATCTTAGAGGTTAACATCCAGATGACGGTGCCGTGCCTGAA 1240 RX 582	0	ThrGlyCysValieuTyrArgTyrGlyThrPheSerThrGluLeuAsnIleValGliGliG		; 3iol.
	<b>.</b>	ATCTTAGAGGTTAACATCATCAGATGACAGACGTCCTGATGCGGGTGCCATGAA		FROM
1241 AGCTCCCTAATAGACTTGGTGACGAGGGAGGAGGTCTGTACC   1300   RT	QD			Youn
	ογ	AGCTCCCTAATAGACTTTGTCGTCACCTGCCAAGGGAGCATTCCCACGGAGGTCTGTACC		organ.
1301 ATCATTTCTGACCCCACCTGCGAGATCACCCAGACCACGTCTGCAGCCCTGTGGATGTG 1360 RA 619 valvalalaAspAlaGluCysArgThrAlaGlnMetGlnThrCysSerAlaValAlaPro 638 RN 1361 GATGAGATGTGTCTGCTGACTGGAGACGTCTGAGGACGTACTGTGTG 1420 RP RS 639 AlaProGlyCysGlnLeuValLeuArgGlnAspPheAsnGlnSerGlyLeuIyrCysLeu 658 RA 1421 AACCTCACCCTGGGGGATGACACGTCTCACGAGCACCCTGATT 1471 RS 659 ARNAISerLeuAlaAsnGlyAsnGlyLeuAlaValAlaSerThrHisValAlaValGly 678 RA	QQ	GlyAsnSerValGluLeuThrValThrCysGluGlySerLeuProGluGluValCysThr		11 R
619 Valvainia	ΟŽ	ATCATTTCTGACCCCACTGCGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTG		ROM
1361 GATGAGATGTGTCTGCAGACCTTCAATGGGTCTGGGACGTACTGTGTG 1420	0			(NOV
639 AlaProGlyCysGlnLeuValleuArgGlnAspPheAsnGlnSerGlyLeuTyrCysLeu 658 RA  1421 AACCTCACCCTGGGGGATGACACACAGCCTCACCTGAGCACCCTGATT 1471 RA  659 AsnValSerLeuAlaAsnGlyAsnGlyLeuAlaValAlaSerThrHisValAlaValGly 678 RA  659 AsnValSerLeuAlaAsnGlyAsnGlyLeuAlaValAlaSerThrHisValAlaValGly 678 RA	δλ	GATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTG		ROM I
1421 AACCTCACCTGGGGATGACACAAAGCCTGGCTCTCACGAGCACCCTGATT 1471 RA	Dp	AlaProGlyCysGlnLeuValLeuArgGlnAspPheAsnGlnSerGlyLeuTyrCysLeu	RX MEDLINE=2 RA Strausber	38825 R.L.
659 AsnValSerLeuAlaAsnGlyAsnGlyLeuAlaValAlaSerThrHisValAlaValGly 678 RA	ζŎ.	AACCTCACCCTGGGGGATGACACAAGCTGGGTCTCACGAGCACCTGATT	RA Klausner RA Altschul	. F. C.
		AsnValSerLeuAlaAsnGlyAsnGlyLeuAlaValAlaSerThrHisValAlaValGly	RA HOPKIDS R RA Diatchenk	F. I.

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pecific gene, Pmel 17, maps near the silver coat color chromosome 10 and is in a syntenic region on human
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Feingold E.A., Grouse L.H., Derge J.G.,
Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Steeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Ardan H., Moore T., Max S.I., Wang J., Hsieh F.,
Aarusina K., Farmer A.A., Rubin G.M., Hong L.,
Dares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .A., AND SEQUENCE OF 25-53.
5; PubMed=8179825;
Keen J.S., Neubauer M., Aruffo A., Hellstroem I.,
Marquardt H.,
oression of the gene for the melanoma-associated ME20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ation and FISH mapping of human Pmel 17, the putative
                                                                                                                                                                                                                                                                                         STANDARD,
2014448; O14817; O16565;
21. 31, Created)
21. 31, Created)
22. 32, Created)
23, Last sequence update)
21. 43, Last sequence update)
22. 43, Last annotation update)
23. 43, Last annotation update)
24. 43, Last annotation update)
25. 43, Last annotation update)
26. 43, Last annotation update)
27. 43, Last annotation update)
28. 49, Last annotation update)
39. 40, Last sequence of the content of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ria; Primates; Catarrhini; Hominidae; Homo.
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tamaneni C., Kozak C.A., Copeland N.G.,
enkins N.A., Barton D., Francke U., Kobayashi Y.,
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8.S., Heng H.H., Shi X.-M., Tsui L.-C., Lee Z.H., on B.S.;
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Boer A.J., Vogel A.M., Loenen W.A., Figdor C.G.;
acterization of the melanocyte lineage-specific
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Rabiting M., Madan A., Rodrigues S., Sanchez A. Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; R. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

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RT "Generation and initial analysis of more than 15,000 full-length human and mouse could represent an elanocytes but overexpressed at low levels of the soluble form, ME20-5, could protect tumor cells from antibody mediated immunity.

"SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL). THERE C. IS ALSO A SECRETED SOLUBLE FORM, ME20-5, PROBABLY PRODUCT OF PROTEOLYTIC CLEAVAGE.

"TISSUE SPECIFICITY: Preferentially expressed in melanomas. Some expression was found in dysplastic nevi. Not found in normal certisuses nor in carcinomas.

C. -: SIMILARITY: EDLONGS TO THE PWEL-17/NMB FAMILY.

--: SIMILARITY: Contains 1 PKD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Transmembrane; Glycoprotein; Signal; Melanin biosynthesis; Repeat;
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Q0; G0:0005886; C:plasma membrane; TAS.
InterPro; IPR000601; PKD.
Pfam; PF00801; PKD; 1.
SMART; SM00089; PKD; 1.
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EMBL; U31797; AAB00386.1; JOINED.
EMBL; U31797; AAB00386.1; JOINED.
EMBL; U12093; AAB18479.1; --
EMBL; U12093; AAB19181.1; JOINED.
EMBL; U19491; AAB19181.1; JOINED.
EMBL; U19491; AAB19181.1; JOINED.
EMBL; BC001414; AAB19181.1; --
PIR; I33490; I33490.
GGREW; HGNC: 10880; SILV.
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EMBL; U31808;
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295 1161 315 1221 328	dy 1281   ICCARGOSTIC	368	388 lyGlySerGlyThrTyrCyFleushanserLeuahaAspalaAspserLeuahaMetv  1458 CGAGCCCTGATTTCTGTTCCTGACAGAGACCAGCCTTTAAGGATGGCAAACA	Db 408 alSerThrGlnLeuValMetProGlyGlnGluAlaGlyLeuÅrgGlnAlaPro- 425 Oy 1518 GTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTTTGG 1574	426	443	2.4	DT 01-DEC-1992 (Rel. 24, Created) DT 01-DEC-1992 (Rel. 24, Last sequence update) DT 01-DEC-1992 (Rel. 22, Last annotation update) DF 10-OCT-2003 (Rel. 42, Last annotation update) DF Protein tyrosine phosphatase, non-receptor type 4 (EC 3.1.3.48) DF (Protein-tyrosine phosphatase MEG1) (PTPase-MEG1) (MEG).		OX NCB1_TaXID=b00; RN [1] RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RA MEDLINE=9128864; PubMed=1648233; RA GU M. York J.D., Warshawsky I., Majerus P.W.;	RT "Identification, cloning, and expression of a cytosolic megakaryocyte RT protein-tyrosine-phosphatase with sequence homology to cytoskeletal RT protein 4.1."; RT protein 4	RL Proc. Natl. Acad. Sci. C.S.A. CO.CO. CO. C. R. (2) RP SQUENCE FROM N.A. RC TISSUE=Colon;	RX MEDLINE=22388257; PubMed=12477932; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Klausner R.D., Collins F.S., Wagner L. Shemmen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L. Schamen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Scapleton M., Soaree M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,	RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., R.M., Cibbs R.A., M. Scherren R.J., Lu X., Gibbs R.A.,	RA VILLAION D.N., Muziny D.N., DOCUMENTON, Nodan A., Rodrigues S., Sanchez A., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Alignment Scores: 4.22e-29 Length: 491 Pred. No.: 436.50 Matches: 124 Score: 40.22\$ Conservative: 63 Best Local Similarity: 26.67\$ Mismatches: 123 Query Match: 10.0\$ Indels: 155 DB: 14 INS-10-039-272-1 (1-2661) x PM17 BOVIN (1-491)	CAGTATTTCC2	Qy 663 ACACTIGGGCCTCAACICAIGGAAGIGACTGTACAGAAGACAIGGACGGGCAIAI 719		OY 780 ACTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACC 821 :::::	QY 822 TICCCAAAGAICICCCCAITAIGITIGAIGACTCCIGGAITCAIGAICCTAGCCACTICCTCA 881	Qy 882 ATTATTCTACCATTACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTT	942		Qy 1050 GA 1051 		Qy 1051Db 195 rpValProThrThrGluAspValGlyThrThrProGluGlnValAlaThrSerLysValL 215	Qy 1051 1051  Db 215 euSerThrThrProValGluMetProThrAlaLysAlaThrGlyArgThrProGluValS 235	Qy 1052	Qy 1079CTGCTGGTGACRACC 1094  Qy 1079	1095 CCCTGGA       275 roThrGl	1124

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201 ICTICIGATGAAAATGACTGGAATGAAAACTCTACCCAGTGTGGAAGCGGGGAGACATG 260
                                                                                   224 AlaargaspGlnSerAsn---AsnGlulleMetIleGlyValMetSerGlyGlylleLeu 242
                                                                                                                                                                                                         321 GCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAG 380
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|GlySerLysPheArgTyrCysGlyArgThrGluValGlnSerValGlnTyrGlyLysGlu 347
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                                                                                                                            261 AGGTGGAAAAACTCCTGGAAGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCA
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                                                                                                                                                                                                                                  ------AACATAGTCTATGAGAAGAACTGC
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                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :-
                                                                                                                                                                                                   tyrosine + phosphate.
-!- SIMILARITY: Contains 1 FERM domain.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzzwinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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TAS
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-!- FUNCTION: May act at junctions between the membrane and
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PHOSPHOCYSTEINE INTERMEDIATE
(BY SIMILARITY).
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DR DR KKW KKW KKW LT FTT FTT FTT FTT FTT FTT SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acetyldihydrolipoamide.

COFACTOR: Concains 1 covalently bound lipoyl cofactor.

SUBUNIT: 20 TO 30 ALPHA(2)-BETA(2) TETRAMERS OF E1 + 6 HOMODIMERS

OF E3 + 60 COPIES OF E2.

SUBCELLULAR LOCATION: Mitochondrial matrix.

DISEASE: PRIMARY BILIARY CIRRHOSIS (PRC) IS AN AUTOIMMUE DISEASE

CHARACTERIZED BY INLYAMMATORY OBLITERATION OF INTRA-HEDRATIC

BILE DUCT, LEADING TO LIVER CELL DAMAGE AND CIRRHOSIS. THE E2

COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX IS THE AUTOANTIGEN FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1988 (Rel. 08, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 41, Last annotation update)
Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
complex (EC 2.3.1.12) (E2) (PDC-E2) (70 kDa mitochondrial autoantigen
of primary biliary cirrhosis) (PBC) (Fragment).
                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                    Titani K., Miyata T.; "Molecular cloning of dihydrolipoamide acetyltransferase of the rat molecular cloning of dihydrolipoamide comparison and evolutionary pyrvate dehydrogenase complex: sequence comparison and evolutionary relationship to other dihydrolipoamide acyltransferases."; Biochim. Biophys. Acta 1131:114-118 (1992)
                                                                                                                                                                                                                                                                                                    Matuda S., Nakano K., Ohta S., Shimura M., Yamanaka T., Nakagawa S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family. SIMILARITY: Contains 2 lipoyl-binding domains.
    1103 CTGAGTAGGATTCCTGATGAAACTGCCAGATTAACAGATATGGC 1147
                   SEQUENCE OF 12-555 FROM N.A., AND PARTIAL SEQUENCE.
                                                                                    Ä.
                                                                                    555
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Interpro; IPR006257; AceF_long.
Interpro; IPR000089; Biotin lipoyl.
Interpro; IPR004167; B3_binding.
                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87196380; PubMed=3571977;
                                                                                                                                                                                                                                                                                     TISSUE=Heart;
MEDLINE=92256482; PubMed=1581353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D10655; BAA01504.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D00092; BAA20956.1; --
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 86-523 FROM N.A.
                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S21766; S21766.
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                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver
                                                                                        ODP2 RAT
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AT------GGGTCTGGGACGTACTGTGTGAACCTCACCCTGGGGGATGACAA 1445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1167 CAATTGTAGAGGGA---ATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGC 1223
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353 isTyrTyrLeuSerValAspValAsnMetGlyGluValLeuLeuValArgLysGluLeuA
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                                                                                                                                                                                                                                                                                                                          DI -> GP (IN REF. 2).
LSCDHRVVDGAVGAQMLABFKKYLEKPVTMLL -> HSAVI
IELWMEQLEPSGLL (IN REF. 2).
3D7A2DCF88DDB794 CRC64;
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                                                                                                                                                                                    E3 AND/OR E1 COMPONENTS BINDING DOMAIN (POTENTIAL).
                                                                                                                              Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
                                                                                                                                                                                                                                CATALYTIC (BY SIMILARITY).
COA-BINDING (BY SIMILARITY)
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Matches:
Conservative:
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InterPro; IPR003016; Lipoyl_BS.
Pfam; PP00198; 2-oxoacid_dh; 1.
Pfam; PF00184; biocin_lipoyl; 2.
Pfam; PF02817; e3_binding; 1.
Propom; PD001115; 2oxoacid_dh; 1.
TIGRPAMS; TIGR01349; PDHac_trf_mito; 1.
PROSITE; PS00189; LIPOXL; 2.
                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                POTENTIAL.
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34.90%
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2.40%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                        379
523
172
528
532
86
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252

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1351

DR Pfam; PF01403; Sema; 1.  DR PRINTS; PR01705; TSPIRREPEAT.  DR SNART; SM00433; PS1; 1.  DR SNART; SM00430; Sema; 1.  DR SNART; SM00430; Sema; 1.  DR SNART; SM00230; TSP1; 4.  EROSITE; PS50092; TSP1; 5.  KW Signal; Transmembrane; Repeat; Multigene: SIGNAL  ET CHAIN 20 1093 SERARHORIN SIFT TRANSMEM 979 999 POTENTIAL.  FT TRANSMEM 979 999 POTENTIAL.  FT DOMAIN 236 518 EXTRACELLULAR  FT DOMAIN 664 713 TSP TYPE-1 1.  FT DOMAIN 664 713 TSP TYPE-1 1.  FT DOMAIN 725 850 TSP TYPE-1 2.  FT DOMAIN 725 850 TSP TYPE-1 2.  FT CARBOHYD 95 997 TSP TYPE-1 5.  FT CARBOHYD 95 997 TSP TYPE-1 5.  FT CARBOHYD 157 157 N-LINKED (GLC FT CARBOHYD 158 158 158 158 N-L	Alignment Scores:	511 201 522 239 242 542 561
193   albendard   19497   CGCCTTTAAGGATGGCAAAC   1959   Los   Lo	Mariyota; Meta Mariyota; Duthe U. TaxID=1009 UUENCE FROM NO PAIN=MRI; PLINE=9641443 MARI; Deta MARI; Deta	This SWISS-PROT entry is copyr between the Swiss Institute of the Buropean Bioinformatics to the Buropean Bioinformatics use by non-profit institution modified and this statement is entities requires a license agor send an email to licenselsis.  EMBL; X97818; CAA6538 11;

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ATTICCTGGGATTICTGCTCCTGGCTGC 103
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|PheValGlyLeuSerAsp-ArgValLe 491
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ctSerLeuTrpIleGlnAsnIleThrTh 542
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ySerCysLeuCysArgAlaArgSerCy 581
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family; Neurogenesis;
                                                         5B.
AR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                               Codgulation cascade.

SUBCELLIDIAR LOCATION: Secreted.

TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma. DOWALN: In addition to having a high His and Pro content, this protein has many internal repeats. 12 tandem repetitions of a 5-residue sequence (GHBPH, consensus) form a histidine-rich region. SIMILARITY: Contains 2 cystatin-like domains.
                                                                                                                                                                                                                            "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-: FUNCTION: The physiological function is not yet known. It binds heme, dyes and divalent metal ions. It can inhibit rosette formation and is known to interact with heparin, thrombospondin, and the lysine-binding site of plasminogen. On the basis of its homology with HWW kininogen, the His-rich region of this protein may mediate the contact activation phase of intrinsic blood
glycoprotein (HRG) gene: genetic mapping and in situ localization of HRG to chromosome 3q28-q29.";
Genomics 19:195-197(1994).
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(POTENTIAL).
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(POTENTIAL).
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SIGNAL
                                                                                                                                                                Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HISTIDINE-RICH GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> S (in dbSNP:3181917)
FTIG=VAR 014528
A2B124D6CE93114F CRC64;
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Mismatches:
Indels:
Gaps:
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CYSTATIN-LIKE 2.
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BY SIMILARITY.
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                                                                                                                                     MEDLINE=93092937; PubMed=1459097;
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EMBL; AB005803; BAA21613.1; -.
EMBL; Z17218; CAA78925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000010; Cystatin. Pfam; PF00031; cystatin; 1. SMART; SM00043; CY; 2.
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Genew; HGNC:5181; HRG.
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Pred. No.:
                                                                                             SEQUENCE
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  RRENE REPRESENTATION OF THE PROPERTY OF THE PR
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Best Local Similarity: Query Match: DB:

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1064 ACCCCTICTTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGAGTAGGATTCCTGATGAA 1123
                                          CCACCCAGACCTTCAAAACCC 1063
                                                   CATCCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTT 1257
                                                                                                                                                                                                                                                                                                                                  1258 TGTCGTGACCTGCCAAGGAAGATTCCCACGGAGGTCTGTACCATCATTTCTGACCCCCAC 1317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---HisHisProHisGly 403
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---PheGlnAspTyrGlyProCysAspProProProHisAsnGlnGlyHisCysCysHis 429
                                                                                                                                                                              326 SerCysGlnHisAlaThrPheGlyThrAsnGlyAlaGlnArgHisSerHisAsnAsn
                                                                                                                                                                                                             -----CTTTCAAGCCAC---CATCACAATTGTAGAGGGAATCTTAGAGGTTAACAT
                                                                                                                                                                                                                                346 SerSerAspLeuHisProHisLysHisHisSerHisGluGlnHisProHisGly---His
                                                                                                                                                                                                                                                                                                                                                                          ----ProHis
                                                                                                                                                                                                                                                                                                                                                                                          1318 CTGCGAGATCACCCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTGTCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1378 GACTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGAACCTCACCTCACCTGGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Aczonin, a 550-kd putative scaffolding protein of presynaptic active zones, shares homology regions with rim and bassoon and binds profilin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            090XX7; 090XX6; 090ZJ0; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Piccolo protein (Presynaptic cytomatrix protein) (Aczonin) (Brain-drived HLMN protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99439764; PubMed=10508862;
Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., SUBCELLULAR LOCATION, ALTERNATIVE SPLICING, IISSUE SPECIFICITY, AND INTERACTION WITH PROFILIN.
                                                                                                                                                                                                                                                                                                                                                      374 ---HisAspThrHisArgGlnHisProHisGly------HisHis-
                                                                                                                              -----ProMetSerCysSer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kilimann M.W.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                      HisProHisAlaHisProHisGlu-------
                                                                                                                                                                                                                                                                                                                                                                                                                       -----GlyHisHisProHisGlyHisHisProHisGly-
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US-10-039-272-1 (1-2661) x HRG_HUMAN (1-525)
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SEQUENCE OF 4502-4682 FROM N.A.
                                CCGCCACCGCCACCA
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                                                                                                                      317 ProproLeuLeu-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "IsoId=09QYX7-2; Sequence-VSP_003928, VSP_003929;
-!- TISSUE SPECIFICITY: Highly expressed in brain. Low levels found in stromach. Not detected in other tissues analyzed including adrenal gland, testis and pancreas.
-!- DOWAIN: c2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high specificity and induces a large conformational change.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 X 10 AA TANDEM APPROXIMATE REPEATS OF P-A-K-P-Q-P-X.
Q4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R MGD; MGI:1149390; Pelo.

R MGD; MGI:1149390; Pelo.

R MGD; MGI:1149390; Pelo.

R GO; GO:0005509; F:calcium ion binding; ISS.

R GO; GO:0005509; F:calcium—dependent phospholipid binding; ISS.

R GO; GO:0005524; F:calcium—dependent phospholipid binding; ISS.

R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R F GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.

R R GO; GO:0007010; P:cytoskeleton organization and bi
                                                                                                       MEDLINE=22384373; PubMed=12401793; Kashima Y., Matsumoto M., Fujimoto K., Shibasaki T., Yokoi N., Kashima Y., Matsumoto M., Sasaki T., Tajima N., Iwanaga T., Seino S.; Sasaki T., Tajima N., Iwanaga T., Seino S.; Piccolo, a Ca2+ sensor in pancreatic beta-cells. Involvement of cAMP-GBFII.Rim2.Piccolo complex in cAMP-dependent exocytosis."; J. Biol. Chem. 277:50497-50502(2002).
-!- FUNCTION: May act as a scaffolding protein involved in the organization of synaptic active zones and in synaptic vesicle
                                                                                                                                                                                                                                                                                                                                                       -!- SUBBULT: Interacts with Rabacl/Pral, RIMS2 and profilin.
        Huang W., Jin W., Huang C., Chen B., Zhang J., Ju G.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                 synaptic junctions.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9QYX7-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, Y19185; CAB60731.2; --
EMBL, Y19186; CAB60732.2; --
EMBL; AF181269; AAD55786.2; --
HSSP; P04410; 1A25.
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DOMAIN 371 470
                                                                                                 INTERACTION WITH RIMS2
                                                                                                                                                                                                                                                                                                                                            trafficking.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1;
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ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=90218040; PubMed=2324710;
MEDLINE=90218040; PubMed=2324710;
Ding S., Keese P., Gibbs A.;
"The nucleotide sequence of the genomic RNA of kennedya yellow mosaic "The nucleotide sequence of the genomic RNA of kennedya yellow mosaic tymovirus-Jervis Bay isolate: relationships with potex- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2280 GlyLeuProValSerThrHisProSerLysSerHisProPheArgSerSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCCTGTTTGTTTCCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                986 AGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCGCCACCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Gen. Virol. 71:925-931(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
RNA replicase polyprotein (EC 2.7.7.48).
Kennedya yellow mosaic virus (strain Jervis bay) (KXMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tymoviridae;
                                              5
                                                                                                                                                      DADA460CF3B40888 CRC64;
                                              TKPTN -> SKRRK (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCAGACCTTCAAAACCCACCCTTCTTTAGGACCTGCT 1084
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23
9
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                                                                       /FTId=VSP 003928.
Missing (in isoform 2).
/FTId=VSP 003929.
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                                                                                                                                                                                                                                                                                                                  Mismatches:
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                                                                                                                                                                                                                                Length:
Matches:
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PIR, JQ0533; JQ0533.1; -
MEROPS; C21.001; -
InterPro; IPR001043; Peptidase C21.
InterPro; IPR001708; RNA dep RNApol2.
InterPro; IPR007095; RNA pol_DS_FS.
InterPro; IPR007095; RNA pol_DS_FS.
InterPro; IPR007094; RNA pol_ESVIT.
InterPro; IPR007094; RNA pol_ESVIT.
InterPro; IPR007094; RNA pol_ESVIT.
Pfam, PP05381; Peptidase C21.
Pfam; PP05381; NA dep RNApol2; IPF0m, PP00978; RNA dep RNAPOL3; IPF0m, PP
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C2 DOMAIN 1.
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111.00
60.38%
43.40%
2.29%
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NCBI_TaxID=36392;
                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
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4922
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                                                                                                                VARSPLIC
                                                                                                                                                                    SEQUENCE
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          DOMAIN
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QY 1436 GATGACAAGCCTC		Db 839 LeuSerAsnSerGlu	OY 1568 CICTIG 1573  Db 859 HisLeu 860		AC 09UQB3; 000379; 015390; DT 28-FBB-2003 (Rel. 41, Cr DT 28-FBB-2003 (Rel. 41, La DT 10-OCT-2003 (Rel. 42, La		Eukaryota; Me Mammalia; Eut NCBI TaxID=96			RT Armadillo family."; RL NeuroReport 8.2008.(1)		RC TISSUE=Brain; RX MEDLINE=99268158; PubMed= RA Lu Q., Paredes M., Medina	Orecchio L., Kosik "Delta-catenin, an			RA MEDLINE=99223289; Pubmed= RA Tanahashi H., Tablira I.; RT "Isolation of human delta				RA Xu D., Liang Y., Rogaeva I RA VunderVere P., Bayne M.L.	KA St George-Hyslop D.H.; RT "Preseniling interact with			RA Patenholz W.W.W.W.W.W.W.W.W.W.W.W.W.W.W.W.W.W.W.
I NP BIND 1002 1009 ATP (POTENTIAL). 2 SEQUENCE 1874 AA; 210029 MW; 72BGDDE57732A2AD CRC64:	<pre>gnment Scores:     0.504 te:     110.50 cent Similarity:     122\$ t Local Similarity:     2.28\$  ry Match:     128\$</pre>	4)	/ 797 CGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCATAATGTTTGATGTC 853	854CTGATTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGG	908 AGCTICGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATCACAGGTAT	968 GTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCA :::   583 LeutisProGludanPheThirLeuSertroMhrawownbrown.u.z	1019 GG	603 SerPro	1031CCACCGCCACCACCACCACCATCAAAACCCACCCTTCTTAGGACCT 1081		643 ThrGlnAlaProSerAlaGlnProThrProGlyGluProLeuLeuAlaProProThrThr 662	1082GCIGGIGAC 1090 663 GluLeuLysProGluSerSerAsnProAsnAsnProAsnProAsnProAsnProAsnAidi.	1091 AACCCCTGGAGTAGGATTCCTGATGAAAACTGCCAGATTAACAGATAAGACAC 1150		TIT	/03 IntserSerShrThrThrProProSerProAsnLeuProLeuGlnPheGlySerlleHis 722	SerProPh	CAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTT	743 ThrAsnThrThrLeuSerLeuLeuProGluProLysPro755	1259 GICGLGACCIGCCAAGGGAGCATTCCCACGGAGGTCTGTACCATTCTGACCCC 1315 756			1376 CTGACTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCGTGGGG 1435	77 LeulyirioargasphnePheProAsnThralaSerPheLeuThrargLeuArgLeuSer 798
FT SQ	Ali. Programmer Per Per Que Due	SO	QV QU	रेठ	Qy Db	VQ Db	δ	අ <u>ධ</u>	A A	ζ	qa 8	ž a	δ	qq	8 8	3 8	Db	8 1	g è	n d	ŏ	qq	ζ, 43	}

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IGGCTCTCACGAGCACC-----CTGATTTCTGTTCCTGACAGA 1486
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                                       || :::|||
euProMetProLysAsnAsnCysLeuThrAlaValAlaProSer 818
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|ulleAspSerValGlyMetSerThrAspLeuLeuThrAlaLeuSer 858
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dast annotation update)
catenin) (Neural plakophilin-related ARM-repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sive junction-associated protein which promotes
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nimura M., Zhang D.M., Levesque L., Yu H.,
a E., Ikeda M., Duthie M., Murgolo N., Wang L.,
... Strader C.D., Rommens J.M., Fraser P.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paffenholz R., Franke W.W.;
"Identification and localization of a neurally expressed member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JFORM 1), AND INTERACTION WITH PRESENILIN 1.
(d=9223106;
ledina M., Ho C., Simmons A.D., Lovett M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a-catenin and its binding specificity with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ordata; Craniata; Vertebrata; Euteleostomi; ...mates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORM 1), AND INTERACTION WITH PRESENILIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on in the brain with a novel member of the
                                                                                                                                                                                                                                                                                                                                                                                                               ; PRT; 1225 AA.
O43206; O43840; Q13589; Q9UM66; Q9UPM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M N.A. (ISOFORM 1), AND INTERACTION WITH
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na M., Zhou J., Cavallo R., Peifer M.,
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187 nLeuProAlaArgGlyThrGlnAlaArgAlaThrGlyGlnSerPheSerGlnGlyThrTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlufhrfhrserAlalleLeuAlaserValLysGluGlnGluLeuGlnPheGluArgLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 Glyśer-diumhrdlyserMetSerSerMetSerSerAladluGluGln-----PheGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       667 TIGGGCCTCAACTCATGGA---AGTGACTGTCTACAGAAGACATGGACGGCATATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 nfrpglnserglnaspolyglnLysaspileGluaspGluLeuThrThrGlyLeu----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 724 CCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            784 TGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAAGATCTCCCCATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrargGluLeuGluAlaGluArgGlnIleValAlaSerGlnLeuGluArgCysLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7. FTTG=VSP_006746.

426 426 V -> D (IN REF. 3, 4 AND 5).

43 443 443 V -> D (IN REF. 3, 4 AND 5).

725 725 P -> A (IN REF. 3, 4 AND 5).

894 894 R -> L (IN REF. 3, 4 AND 5).

909 909 R -> L (IN REF. 3, 4 AND 5).

909 909 A -> V (IN REF. 3, 4 AND 5).

900 900 A -> G (IN REF. 3, 4 AND 5).

1102 1102 A -> G (IN REF. 4).
                                                                                                              1225
87
44
132
141
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Matches:
Conservative:
Mismatches:
Indels:
                                                                  (in isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 n-----LeuAsnSerLysProGlu---
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                                                                      Missing
ARM 7.
ARM 8.
ARM 9.
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110.00
32.43%
21.53%
2.27%
  875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50176; ARM REPEAT; 3.
Cell adheaion; Cytoskeleton; Structural protein;
Developmental protein; Repeat; Coiled coil; Alternative splicing.
DOMAIN 49 84 COILED COIL (POTENTIAL).
                                                                                SEQUENCE OF 543-656 FROM N.A. Wilson R., Smith A., Elliott G., Kramer J., Latreille P., Keppler Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0007158; P:neuronal cell adhesion; NAS.
InterPro; IPR008938; ARM.
InterPro; IPR000225; Armadillo.
Empi, PF00514; Armadillo_seg; 5.
SMART; SM00185; ARM; 7.
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EMBL; U52828; AAB96357.1; -...
EMBL; U81036; BAA36163.1; -...
EMBL; U81004; AAD00453.1; -...
EMBL; U72665; AAB68599.1; -...
EMBL; U52351; AAB97957.1; -...
EMBL; AC003089; AAB88340.1; -...
EMBL; AC003089; AAB88340.1; -...
                 plakoglobin/armadillo multigene family.";
Differentiation 61:293-304(1997).
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POLY-LYS.
ARM 1.
ARM 3.
ARM 4.
ARM 6.
                                                                                                                                                                                       SEQUENCE OF 865-1225 FROM N.A.
MEDLINE=97202103; Pubmed=9049630;
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SEQUENCE OF 873-1225 FROM N.A.
TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:2516; CTNND2.
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                                                                                                                                                                                                                   TGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCACAATTGTAGA 1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1237 TGAAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCACGGAGGTCTG 1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1357 TGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTG 1416
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247 aAlaAlaAlaAlaLeuTyrTyrSerSerStThrLeuProAlaProProArgGlyGlySe 267
                                                                                                                                                                                                                                                                                                                                                                                                            ------SerSerProLysGlnSerProSerArgLeuAlaLysSerTyrSe 312
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                                                                                                                                                                                                                                                                                               --GlyAlaThrTyrAlaAlaProAr
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"Molecular cloning of the amino-terminal and 5'-flanking region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 40-1324 FROM N.A.
MEDLINE=9903932; PubMed=9804771;
Desseyn J.-L., Busine M.P., Porchet N., Aubert J.-P., Laine A.;
"Genomic organization of the human mucin gene MUCSB: cDNA and genomic sequences upstream of the large central exon.";
J. Biol. Chem. 273:30157-30164(1998).
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MEDLINE=99009274; PubMed=9790959;
Offner G.D., Nunes D.P., Keates A.C., Afdhal N.H., Troxler R.F.;
"The amino-terminal sequence of MUC5B contains conserved
multifunctional D domains: implications for tissue-specific mucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Q9HC64; Q00447; Q00573; Q14985; Q15494; Q95291; Q95451; Q14881;
Q99552; Q9UE28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jyhusa, ...
(99552; QyBc28;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Mucin 5 subtype B, tracheobronchial) (High
                                                                                            CCCTTCTTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGAGTAGG
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE OF 1-1594 FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                 r human high molecular weight salivary mucin mucin MUC5B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: Highly glycosylated.
-!- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
-!- SIMILARITY: Contains 3 VWFC domains.
-!- SIMILARITY: Contains 4 VWFD domains.
-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic organization of the 3 region of the human MUCSB mucin.";
"Genomic organization of the 3 region of the human MUCSB mucin.";
"J. Biol. Chem. 272:16873-16883 (1997).
-!- FUNCTION. Salivary mucin that is thought to contribute to the lubricating and viscoelastic properties of whole saliva.
-!- SUBCELLULAR LOCATION. Secreted.
-!- TISSUE SPECIFICITY: Expressed mainly in bronchus glands and also in submaxillary glands, endocervix, gall bladder, and pancreas.
                                                                        "Human mucin gene MUCSB, the 10.7 kb large central exon encodes various alternate subdomains resulting in a super-repeat. Structural evidence for a 11p15.5 gene family.";
                                                                                                                                                                                                                                                                                                                                                        TISSUE=Gall bladder;
MEDLINE=97293229; PubMed=9164870;
Reates A.C., Nunes D.P., Afdhal N.H., Troxler R.F., Offner G.D.;
"Molecular cloning of a major human gall bladder mucin: complete C-terminal sequence and genomic organization of MUCSB.";
Blochem. J. 324:295-303(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Sublingual gland;
MEDINE-96125355; PubMed-8554565;
Troxler R.F. Offner G.D., Zhang F., Iontcheva I., Oppenheim F.G.;
"Molecular cloning of a novel high molecular weight mucin (MG1)
from human sublingual gland.";
Biochem. Biophys. Res. Commun. 217:1112-1119(1995).
                                      Desseyn J.-L., Guyonnet-Duperat V., Porchet N., Aubert J.-P.,
                                                                                                                                                                                                                          Nielsen P.A., Bennett E.P., Wandall H.H., Therkildsen M.H.,
Hannibal J., Clausen H.;
                                                                                                                                                                                     TISSUE=Salivary gland;
MEDLINE=97292540; PubMed=9147051;
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U78552; AAC51344.1; JOINED.
U78553; AAC51344.1; JOINED.
U78551; AAC51343.1;
U95031; AAC51343.1;
Y09788; CAA70926.1;
                     MEDLINE=97166151; PubMed=9013550;
                                                                                                                                                                                                                                                               "Identification of a major human (MG1) as tracheobronchial mucin M
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MEDLINE=97347489; PubMed=9201995;
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EMBL; AF066604; AAC67545.1; --
EMBL; AZ004862; CAA06167.1; --
EMBL; Z72496; CAA96577.1; --
EMBL; X74995; CAA52910.1; --
EMBL; UG3836; AAB61398.1; --
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600770; -.
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....4831 -ThrAlaSerThrValProSerSerThrValG1yThrThrArgThrProAlaValLe 4850
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4785 Thr-ThrIrp---IleLeuThrGluProSerThrIleAlaThrValMetValProThrGl 4803
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4725 ProGluThrThrHisThrSerThrValLeuThrThrThrThTAlaThrMetThrArgAlaThr 4744
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4705 ValproAlaGlnThrThrThrProMetSerThrMetSerThrIleHisThrSerSerThr
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FPGLCN -> LPCLCK (IN REF. 2).

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RT -> TR (IN REF. 2).

C -> P (IN REF. 2).

A -> S (IN REF. 3).

B -> R (IN REF. 3).

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                 F:protein binding; IPI
                            InterPro; IPR006208; Cya knot.
InterPro; IPR006209; Cya knot.
InterPro; IPR006209; Cya knot.
InterPro; IPR006209; TIL_Cysrich.
InterPro; IPR001007; VWE_Inhibitor.
InterPro; IPR001007; VWE_InterPro; IPR00115; VWE_InterPro; IPR00115; VWE_InterPro; IPR00115; VWE_InterPro; IPR00115; VWE_InterPro; IPR00115; VWE_InterPro; IPR00116; VWE_InterPro; IPR00116; VWE_InterPro; IPR00117; VWE_InterPro; IPR0117; VWE_In
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907 GAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGT 954 :::       4887 gAlaPheGlyGlnPhePheSerProGlyGluValileTyrAsnlygThrasnargalag1 4907	CTGC 10	) L	AC 10	uSerSe 494	-	i io	11	97	CATG 123	498	129	66	CCAGAACACAGTCTG 134	501	781	502 h		5027 eAspGlyThrSerTyrThrPheArgGlyAsnCysThrTyrValLeuMetArgGluIleHi 5047	144	Th 506	1445AGCCTGGC 1452	508	CC	5087 lLeuThrValThrMetValHisGlyLysGluGluGlyLeuIleLeuPheAspGlnIlePr 5107	7 7	5107 oValSerSerGlyPheSerLysAsnGlyValLeuValSerValLeuGlyThrThrThrThrMe 5127		3lyValThrValThrPheAsnGlyGlnValPheGlnAl 514	-	GlyGlnCysGlyThrCysThrAs 516	1659	5167 nAsnGlnArgAspAspCysLeuGlnArg 5176	LT 15 HUMAN IRPS HUMAN STANDARD; PRT; 427 AA. Q14653; 01-NOV-1997 (Rel. 35, Created)
ζζ OD	δλ	qq	λ̈	gg	δ,	අුර	δ	qq	8	a a	δλ	qq	δy	Db	Οy	qu	ζζ	qq	δλ	ПЪ	ζŏ	QQ	δy	qq	δλ	QQ	Qy	qq	δλ	Db	Qy	gg	RESULT IRF3 HU ID IR AC Q1 DT 01

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SEQUENCE OF 323-413 FROM N.A.

MEDLINE=99020108; PubMed=9803267;

Bellingham J., Gregory-Evans K., Gregory-Evans C.Y.;

Mapping of human intraferion regulatory factor 3 (IRF3) to chromosome 19q13-3-13-4 by an intragenic polymorphic marker.";

Ann. Hum. Genet. 62:231-234(1998).

-! FUNCTION: MAY ACTIVATE TRANSCRIPTION BY COMPLEX FORMATION WITH OTHER TRANSCRIPTIONAL FACTORS, POSSIBLY MEMBERS OF THE STAT FAMILY. BINDS SPECIFICALLY TO THE IPN-STIMULATED RESPONSE ELEMENT (ISRE) BUT NOT TO THE IRP-1 BINDING SITE PRD-1.

-! SUBCELLULAR LOCATION: Nuclear.

-! TISSUE SPECIFICITY: Expressed constitutively in a variety of
                                                                                                                                            TISSUE-Retina;
MEDLINE=96102173; PubMed=8524823;
Au W.W.-C., Moore D.P.A., Lowther W.W., Juang Y.-T., Pitha P.M.;
"Identification of a member of the interferon regulatory factor family that binds to the interferon-stimulated response element and activates expression of interferon-induced genes.";
Proc. Natl. Acad. Sci. U.S.A. 92:11657-11661 (1995).
                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Transcription regulation; DNA-binding; Nuclear protein; Activator;
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R -> Q (in dbSNP:968457).

/FTId='VAR 011901.

/FTId='VAR 011902.

S -> T (in dbSNP:7251).

/FTId='VAR 011902.
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F536676FA78B0110 CRC64;
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90
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interferon regulatory factor 3 (IRF-3).
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Mismatches:
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Matches:
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ProDom; PD002355; IRF; 1.
SMART; SM00348; IRF; 1.
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EMBL, U86636; AAC68818.1; -.
HSSP; P23906; 2IRF.
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                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=9606;
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Best Local Similarity:
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Query Match DB:		2.20%	HO ,	133 18	
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op qu		 	:::::    uArgGlnAspAlaGl1		
QY	440 TGCTGAT	CCATATGTTTACAACT	GGACAGCATGGTCAG	TGCTGATCCATATGTTTACAACTGGACATGGTCAGAGGACAGTGACGGGGAAAATGG 499	0
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qa	60 arhrely	d	AlaTyrValProGlyA	, ulo	ก
à i		ATGGAGAAGATGGAATTTCAT		CTACGICTICCACA 59.	94
g :	n u	riiphysaigasminenty. CacthggtCaGTATTTCCa		GAAATTGGGACGATGTTCAGTGAGAGTTT 64	12
ž 8	2 4	 gserLysAspProHis	::: AspProHisLysIleT	uaspargSerLysAspProHisAspProHisLysIleTyrGluPheValAsnSerGlyVa 11	4
٥٨	643 CTGTGAP	ACACAGCCAATGTGAC	ACTTGGGCCTCAACTC	CTGTGAACACCAATGTGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAA 70	22
qq	::: 114 lGlyAsF	: pPheSerGlnProAsp'	   ThrSerProAspThr#	snglygly 12	53
δλ	703 GACATGO	GACGGCATATGTTCC	CATCGCACAAGTGAAA	TGTACGTGGTAACAGATC 7	62
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ζ	823 TCCCAA	AGATCTCCCCATTATG	<b>TTTGATGTCCTGATT</b> (	CCCAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAA 8	00
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ζ	943 CAATCA	NTACTGTGAATCACACG	tatgtgctcaatgga 	AACCTCAC	002
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ò	1003 GAAAGC	CTGCAGCACCAGGACCT	TGTCCGCCACCGCCA	GAAAGCTGCAGCACCAGGACCTTGTCCGCCACCGCCACCACCACCAGACCTTCAAAACC 1	1062
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ò	1063 CACC	CCTTCTTTAGGP	CCTGCTGGTGACAAC	CACCCCTTCTTTAGGACCTGCTGGACAACCCCCTGGAGCTGAGTAGGATTCC	1116
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Š	1117 TGATGA	TGATGAAAACTGCCAGATTAACAGATATGGCCAC-	CAGATATGGCCAC		1158
qq	198 oglydi	lúGluTrpGluPheGlu	ıValThrAlaPheTyı		218
ζō	1159 CACCAT	rcacaattgtagaggg	AATCTTAGAGGTTAAC		1218
Db	218 nThr1]	leserCysProdludly	LeuArgLeuvalGly		37
δý	1219 GATGCCG	1	-GIGCCAIGGCCIGAA	-GIGCCAIGGCCIGAAGCICCCIAAIAGAC	1255
qu	237 rLeuP	euProGlyTrpProValTh:	rLeuProAspProGly	ProvalThrLeuProAspProGlyMetSerLeuThrAspArgGlyVa	257
δλ	1256	TTTGTCGTGACCTGCCAAGGG		12	
qq	257 IMetS	erTyrValArgHisVa	iLeuserCysLeuGl)	7 269	

Search completed: September 10, 2004, 15:41:24 Job time : 87.5 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

September Run on:

9, 2004, 20:27:32; Search time 16423 Seconds (without alignments) 7022.822 Million cell updates/sec

Title: Perfect score:

Scoring table: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

6940544 Total number of hits satisfying chosen parameters:

3470272 segs, 21671516995 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

GenEmbl:\*

9b htg.\*
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## ALIGNMENTS

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linear	HGFIN MRNA,					
2662 bp mRNA	Homo sapiens transmembrane glycoprotein HGFIN mRNA,		AF322909.1 GI:11993664		ns (human)	ST
AF322909	Homo sapie	AF322909	AF322909.1		Homo sapiens (human)	Homo sapiens
RESULT 1 AF322909 LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM

PRI 23-APR-2003 complete cds.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2662)
Bandari,P.S., Qian,J., Yehia,G., Joshi,D.D., Maloof,P.B.,
Potian,J., Oh,H.S., Gascon,P., Harrison,J.S. and Ramesiwar,P.
Hematopoietic growth factor inducible neurokinin-1 type: a

REFERENCE AUTHORS

TITLE

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185 South Orange Ave, MSB, Rm. E-579, Newark, NJ 07103, USA
Location/Qualifiers
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/organia="Homo sapiens"
/organia="mRNA"
/db_xref="taxon:9606"
/tissuc_type="bone marrow peripheral blood"
/oote="hematopoietic growth factor-inducible:
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Rameshwar, P.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0306828-A 8 21-AUG-2003;
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/ mol type="unassigned DNA"
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Db 2270 TGATGGACCATAACGGCCCAAGCCTGTGATGTGCCACCTGCTAGACCAAA 2329  Qy 2271 AAATACTACTCCTAATGGGTGGTATTTTGGTGCACACTTGCTTG	RESULT 8 AX362281 CORGANISM CORGA
	551 TTGTCACT 611 ATAGTCCT 611 ATAGTCCT 670 ATAGTCCT 671 CCGTGTTC 730 CCGTGTTC 730 GAGTTTCC 731 GAGTTTCC 731 GAGTTTCC 731 TTTGGGG 1911 TACTGCAG 1970 TACTGCAG 1971 TTCATTA 2030 TGTCCCG 2091 GAAGAGG 2091 GAAGAGG 2151 GTTTCT 2150 GAAGAGG 2151 GTTTCT 2210 GTTTCT 2211 TGATGT 2211 TGATGGT 2211 TGATGT

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1311 ACCCCACCTGCGAGATCACCAGAACACTCTGCAGCCCTGTGGATGTGGATGTGT   1370	TGACAACCTACTTGCTTGGCTG 233  TGACAACCTACTTTGCTTGGCTG 238  TGACAACCTTTAGTTAGTGCTTTTTA 239  GACATTTAGTTAGTGCTTTTTA 239  GACATTTAGTTAGTGCTTTTTA 244
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ORIGIN  Query Match Query Match Best Local Similarity 97.8%; Pred. No. 0; Matches 2576; Conservative 0; Mismatches 20;  Qy 28 AACCTTGGTGCCTGCGTCGTGAGAATTCAGCATGGAATGT Ob 50 ACCTTGAGGGCTGCGTCGGTGAAATTCAGCATGGAATGT	88 110 148	170   GCAALGAARACTICISCIANA   170   GCAALGAARACTICISCIANA   170   GCAALGAARACTICISCIANA   170	150   196GCTCAAATATAACATTTGCGGGGGGGGGGGGGGGGGGGG	Oy 508 AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCC	8 9 S S S S S S S S S S S S S S S S S S	Oy 628 GTTCAGTGAGATTTCTGTGAACAGCCAATGTGACACT	688	Qy 748 ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTAGTT 	Qy 808 CATCCGACGAAACCTTCC-CAAAGATCTCCCCATTATGT'	OY 867 CIAGCCACTTCCTCAATTATTCTACCATTAACTACAGT( D) 890 CIAGCCACTTCCTCAATTATTCTACCATTAACTACAAGT(	QY 927 GCCTGTTTGCACCAATCATACTGTGAATCACGT. Db 950 GCCTGTTTGTTTCCACCAATCATGTGAATCACGGAATCACACGAATCACACGAATCACACGAATCACACGAATCACACGAATCACACGAATCACACGAATCACACACGAATCACACACA	QY 987 GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTT
2450 IATACCAGGCATGATGACACTCTTGTGTATATTCCAAATTTTGTACAGTCG 2509 2451 CTGCACATATTTGAAATGAAATTTAAGACTTTCCAAAATTTTTGTACAGTCG 2509 2451 CTGCACATATTTGAAATCAAAATTAAGACTTTCCAAAATTTGGTCCCTGGTTTTTCA 2510 [	2569 IGGCAACTIGATGAAAGATTTTCACTIGTTTTTTTTTTTT	AY359124 LOCUS LOCUS LOCUS LOCUS LOCUS AY359124 AY359124 AY359124 Homo sapiens clone DNA125214 NMB (UNQ1725) mRNA, complete cds. DEFINITION Homo sapiens clone DNA12514 NMB (UNQ1725) mRNA, complete cds. AY359124	Mammalia; bulletia; Filmacos, Carlos, Baker, K., Baldwin, D., Brush, J., AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Cur, Q., Hass, P.E., Dowd, P., Eaton, D., Foster, J., Cfiimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, B., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Sinkh, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,	Goddard, A., Wood, W.:. alu Goudwar, F.:  TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment	AL CE RS	Direct Submi Submitted (O Inc., 1 DNA Loc	rce	gene 12683 /locus_tag="UNQ1725" CDS 821800 /locus_tag="UNQ1725"	/note="PRO9925" /note="PRO9925" /codon_start=1 /product="NMB" /nrotein_id="AA089481.1"	/db_xref="d1:37183364"   translation="MECLYYPGFLLLAARLPLDAAKRFHDVLGNERPSAYMREHNQL   NGWSSDENDWIEKLYPVWKRGDMRWKOSWKGGRVQAVLTSDSPALVGSNITFAYNLIF   DPCOKEDANGATVYEKNCRNBAGLSADPYYYWWTAWSEDSDGENGTGQSHHVVFPDGK	PEPHHPGWRRWNFIYVPHTLGQYFQKLGRCSVRVSVNTANVTLGPQLMEVTVYRRHGR AYVPTAQVKDVYVVTDQIPVFVTMFQRNDRNSSDETFLKULPINFDVLIHDFSHFLNY STINYRYRSFGDNTGLFVSTNHTVNHTYVLNGTFSLMLTVKAAAPGPCEPPPPRPSK PTPLSKSFGDNTGLFVSTNHTVNHTYVLNGTSLMLTVKAAPGRCEPPPPRPSK	IQMIDVIMPVPWPESSLIDFVVTCQGSIPTEVCTIISDPTCETTQNTVCSPVDVDEMC ILTVRRTFNGSGTYCVMLTLGDDTSLALTSTLISVPDRDPASPLRMANSALISVGCLA ILTVRTTSLLVYKKHKEYNPIENSPGNVVRSKGLSVFLNRAKAVFFPGNQEKDPLLKNQ EFKGVS"

TTGTCCGCCACCGCACCACCAC 1046 TTTGATGICCTGATICATGAIC 866 TATGTGCTCAATGGAACCTTCA 986 CTTGGGCCTCAACTCATGGAAG 687 TGGAGCTTCGGGGATAATACTG 926 ATCGCACAGTGAAAGATGTGT 769 ITCCAGAAGAACGATCGAAATT 807 747 ARGCTGGTTTATCTGCTGATC 447 CTCACCACCCCGGATGGAGAA 567 TATTTCCAGAAATTGGGACGAT 627 ACCECE SAAATGECACCECC 507 ACGGGGAAATGGCACCGGCC 529 STOTCTACTATTTCCTGGGAT 87 147 169 207 229 ccagreacreaceaecerce 327 CCAGTGACTCACCAGCCCTCG 349 AGCGGGGAGACATGAGGTGGA 267 289 ATCCCACAAGTCAAAGATGTGT AATTAAATGGCTGGTCTTCTG Indels 39; Gaps Length 2683;

		OY 2331 AGTGAAGGATGATATTCATATATTCATGATCATGGACATTTAGTGCTTTTTA 2390	01 01 01 01	OY 2571 TAGACAAGACATTTTTTTTTTTCTTCCTGAAAA-AAAATGAGGGAAGAGACA 2624	10 38 AX677 TION Seque ION AX677 N AX677 DS	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AUTHORS Legrain,P. and Daviet,L. TILE Protein interactions in adipocytes JOURNAL Patent: WO 02086122-A 516 31-OCT-2002; FRATURES Location/Qualifiers Source 11683 //oranism."Homo saniens"	/mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 62.8%; Score 1671; DB 6; Length 1683; Best Local Similarity 99.9%; Pred. No. 0; Matches 1682; Conservative 0; Mismatches 0; Indels 1; Gaps 1; Qy 60 AIGGAAIGICICIAATIICCIGGGAITICIAGAAIGAAIGAAIGH	09	
47 CCAG       70 CCAG 75	1131 AGATTAACAGATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAAGAGG 1190 1190 AGATTAACAGATATGGCCACTTTCAAGCCACCACCATCACAATTGTAGAGGGAATCTTAGAGG 1249 1191 TTAACATCATCAGAGTGACAGAGGCCTGCAGAGGCCTGGAAGCTCCCTAA 1250 1151 TTAACATCATCAGAGGCTGCCAGAGGCCCTGCAAGCTCCCTAA 1250 1250 TTAACATCATCCAGATGACAGACGTCCTGATGCCGGTGCCATGAAGGTCCCTAA 1309	37ACCATCATTTCTG 131	71 GTCTGCTGACTGAGACGTTCAATGGGTCTGGGACGTACTGGATGG 30 GTCTGCTGACTGGACGTACTTCAATGGGTCTGGGACGTACTGTGTGAACC 31 TGGGGGATGACTGCTCAATGGGTCTGGGACGTACTGTGTGAACC 31 TGGGGGATGACACAAAGCCTGGCTCTCACGAGCACCTGATTTCTGTTCTGTACTGACACACAC	491 CAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGCCTGGCCATAT	1551 TYGTCACTGTGATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAA 1610 1610 TYGTCACTGTGATCTCCCTTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAA 1669 1611 ATAGTCCTGGGAATGTGGTCAGAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAG 1670 1671 ATAGTCCTGGGAATGTGGTCAGAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAG 1670 1670 ATAGTCCTGGGAATGTGGTCAGAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAAG 1729	1671 CCGTGTTCTTCCCGGGAAACCAGGAAAGGATCCGCTACTCAAAACCAAGAATTTAAAG 1730		1851 TITGGGGAAGITGAAITTITTATAGGITAAATGICAITITAGAGAIGGGGAGAGAGAITA 1910 	TICAGCCAIGTIGIGAAACIGATAAAAGCAACTTAGCAAGGCTTCTT 197	30 TTCA	60

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1201 GTCGTGACCTGCCAAAGGAGCATTCCCACGGAGGTCTGTACCATTTTCTGACCCCCACC 1260	RESULT 11  ROG61725  BC061725  BC061726  BC061
	220 GTTCCCATCGCACAAGTGAAAGATGTGTACGTGATAACAGATCAGATTCTGTGTTTGTG 779 661 GTTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCCTGTGTTTGTG 720 180 ACTATGTTCCAGAAGTGAAAGATTCATCGACGAAACCATCCAGAATTCTTGTGTTTGTT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: nisc_mgo@nhgri.nih.gov
Akhter.N., Ayele.X., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakeslev,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brocks,S.,
Blakeslev,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="meslcgylvelilaagleploaakrfrdylgheoypdhmrennol
RGWSSDENEWDEOLYPVWRRGEGRWKDSWEGGRVQAALTSDSPALVGSNITFVVNLVF
PRCQKEDANGNIVYERNCRSDLELASDPYVYNWTTGADDEDWEDSTSQGGHLRFPDGK
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AXIPISKVKDVYVITDQIPIFVTMYQKNDRNSSDETFLRDLPFFRDVLHDPSHFLNY
SAISYKWNFGDNTGLFVSNNHTLNHTYVLNGTFNFNLTVQTAVPGPCPSPTPSPSSST
SPSPASSPSPTLSTPSPSLMPTGHKSMELSDISNENCRINRYGYFRATITIVDGILEV
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LCLLSVRRAFNGSGTYCVNFTLGDDASLALTSALISIPGKDLGSPLRTVNGVLISIGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 137 Row: c Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18959233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAMFVTWVTILLYKKHKTYKPIGNCTRNVVKGKGLSVFLSHAKAPFSRGDREKDPLLQ
                               Direct Submission
Submitted (05-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41
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                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeff Green/Paturu Kondaiah, NCI.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Neb site: http://www.nisc.nih.gov/
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NCI_CGAP_F159, 39, 42"
/clone lib="NCI CGAP_F19"
/lab_host="DH10B"
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/protein_id="AAH61725.1"
db_xref="GI:38197644"
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Pred. No. 3.8e-248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
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/note="PKD; Region: Repeats
(PKD1) and other proteins"
/db_xref="CDD:smart00089"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="RGD:71008
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Best Local Similarity 74.1
Matches 1405, Conservative
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PN JP 2001505761-A/3

PD 08-MAY-2001

PF 23-MAY-1997 UP 1997542986

PR 24-MAY-1996 US 60/018228,23-AUG-1996 US 60/023442 PI

PR 24-MAY-1996 US 60/018228,23-AUG-1996 US 60/023442 PI

MICHELE SANICOLA NADEL, JOSEPH V BONVENTRE, CATHERINE A HESSION, PI

TAKAHARU ICHIMURA, HENRY WEI, RICHARD L CATE

PC C12011/21, C1207K14/47, C12N15/62, C07K16/18, A61K38/16, G01N33/50, PC C1201/68,
PC C1201/68,
PC C1201/21, C12N5/10, C12N5/12, A61K48/00

CC Strandedness: Single,
CC Topology: Linear;
FH Key

FT CDS

FT CDS

FT CDS
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RGWSSDENEWDEHLYPVWRRGDGRWKDSWEGGRVQAVLTSDSPALVGSNITFVVNLVF
RCQKEDANGNIYYERNCRNDLGLTSDLHYYNWTAGADDGDWEDGTSRSQHLRFPDRR
PPRRPHGWKKWSFVYFHTLGQYFQKLGRCSARVSINTVNLTAGPQWWEYTVERRYGR
AYIPISKYKDYYYIPDQIPVFYTWSQKNDRNLSDEIFLNDLFIVPULIHDSBHFLND
SAISYKWNFGDNTGLFVSNNHTLNHTYVLNGTFNLNLTVQTAVPGPCPPRSPSTPPPP
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DGLCLLSVRRAFNGSCTYCVNFTLGDDASLALISTLISIPGKDPDSPLRAVNGYLISI
GCLAVLVTWYTILLYKKHKAYKPIGNCPRNTVKGKGLSVLLSHAKAPFFRGDQEKDPL
LQDKRPLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 2279)
Shikano,S., Bonkobara,M., Zukas,P.K. and Ariizumi,K.
Molecular Cloning of a Dendritic Cell-Associated Transmembrane Protein, DC-HIL, that Promotes RGD-Dependent Adhesion of Endothelial Cells Through Recognition of Heparan Sulfate
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ITAM, similar to Mus musculus numb product encoded by
GenBank Accession Number AJ251685"
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                                                                                                                                                                                                                                                                                              AF322054 2279 bp mRNA linear ROD 01-MA Mus musculus dendritic cell-associated transmembrane protein precursor (Dchil) mRNA, complete cds.
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Pred. No. 8.3e-248;
0; Mismatches 442; Indels 54;
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Shikano,S. and Ariizumi,K.
Direct Submission
Submitted (16-NOV-2000) Dermatology, University of Te
Southwestern Medical Center, 5323 Harry Hines Blvd.,
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/strain="BALB/c"
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/db_xref="GI:13172897"
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Location/Qualifiers
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Matches 1409; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 2299;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 1049.8; DB 10; Lengt
Pred. No. 8.4e-248;
); Mismatches 442; Indels
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                                                                                                                                 854. .1039
/note="PKD; Region: Repeat:
(PKD1) and other proteins"
/db_xref="CDD:smart00089"
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Scheetz, T.E., Brownstein, W.J., Usdin, T.B., Toshiyuki, S.,
Garninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKearnan, P.J.,
McKearnan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lul, K., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
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AYIPISKWADYYYITDQIPVFVTMSQKADRALSDEIFLRDLPIVFDVLIHDEBHFLND
SALSYKMANFGDNTGLFVSNNHTLNHTYVLMGFRNLLZVQTAVPGPCPPSSTPPPP
SALSYKMANFGDNTGLFVSNNHTLNHTYVLMGFRNLLZVQTAVPGFPPPSSTPPPPP
STPRSPEPPSELPTITTSPSPSTMSTKSMELSDISNENCRINYGYFRATITIVGGIL
EVSIMQIADVPMPTPQPANSLMDFTVTCKGATPMEACTIISDPTCQIAQURVCSPVAV
DGLCLLSVRRAFNGSGTYCVNFTLGDDASLALTSIISIPGKDPDSPLRAVNGVLISI
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RGWSSDENEWDEHLYPVWRRGDGRWKDSWEGGRVQAVITSDSFALVGSNITFVVNLVP
PRCQKEDANGNIVYEKNCRNDLGLTSDLHVYNWTAGADDGDWEDGTSRSQHLRFPDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (02-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 43 Row: d Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="glycoprotein (transmembrane)
/protein id="AAH26375.1"
/db_xref="GI:20071339"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://mgc.nci.nih.gov
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/clone="MGC:31111 IMAGE:4164706"
/clone="MGC:31111 IMAGE:4164706"
/clone=Ibe="NGT CAAP_SG2"
/lab_host="DH10B"
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/strain="FVB/N"
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Strachan, L., Sleeman, M., Abernethy, N.,
Murison, G.

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Search completed: September 10, 2004, 07:08:45 Job time : 16437 secs

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Oy         312 GACTCACCAGCCCTGAGGGTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGA           Db         1	Db 93 SerginiysValLeuProAspGlyGlnValIleTrpAlaAsnAshThrileIleAshGly Qy 429 GCTGGITTATCTGCTGATCCATATGTTTACAACTGGACAGGACA	113	Qy 489 GGGGAAAATGGCACCGACCAACGTCATAACGTCTTCCCTGATGGGAAACCTTTTCCT	QY 549 CACCACCCGGAIGGAGAAGAIGGAATTICATCTACGICTICCACACACACAGAITICAGIAT	140	Oy TICOAGAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACGGCCAATGTGACACTT  Db 160 TrpGlrvalLeuGlyGlyProValSerArgSerSerTleAlaThrArgHisAlaLvsLeu	Qy 669 GGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATGTTCCC	726	Db 200 LeuAlaHisAlaSerSerThrPheThrIleThi	OY 786 TICCAGAAGAACGAICGAAATICAICGAAGAAACGAAAACCAICAAACAAACGAAAACGAICGAAAAACCAAAAACAAAAACAAAAAAAA	830 GATC		QY 890 ACCATTAACTACAAGTGGAGCTTCGGGGGATAATACTGGCCTGTTTGTT	Db 255 AspLeuSerTyrThrTrpAspPheGlyAspGlyThrGlyThrLeuIleSerArgAlaLeu	QY 950 ACTGTGAATCACACGTATGTGCTCAATGGGAACCTTCAGCTTAACCTCACTGGAAAGCT	0 7 7	OY 1010 GGA	Qy 1012	Db 315 ProThrAlaGluAlaProGlyThrThrSerArgGlnGlyThrThrThrLysValValGly	Qy 1013GCACCAGGACCTTGTCCGCCACGCCACCA		Oy 1042	1043	Db 375 ThrLeuAlaGluValSerThrThrGluGlyThrGlyThrThrProThrArgProSerGly	1058	Db 395 ThrThrValAlaGlnAlaThrThrThrGluGlyProAspAlaSerProLeuLeuPro

----AACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACC 1162 AATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATG 1222 GCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATT 1282 GGAGGTCTGTACCATCATTTCTGACCCCACCTGCGAGATCACCCAGAACACAGTC 1342 CCCTGTGGATGTGGATGTGTCTGCTGACTGTGAGACGAACCTTC---AAT 1399 researcharctersaaccreaccressearsaaccrescresse 1459 CCTGATTTCTGTTCCTGACAGAGACCCCAGCCTCGCCTTTAAGGATGGCAAACAGT 1519 SATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATC-----TCCCTCTTG 1573 ---CCAATAGAA 1609 ICCTGGGAATGTGTCACAAAGCCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAA 1669 |||||||:::||| pileValGinGly-------ileGluSerAlaGluIleLeuGln 467 nSerSerThrGlySerlleSerProLeuLeuAspAspThrAspThrIleMetLeu 433 ||| ::: :::
nSerValProProSerProAspCysGlnLeuValLeuWalLeuLysGly 527 | ::: |||||| :::||| rGlnLeuValValProGlyGlnAspGlyGly-------LeuGlyGln 562 ::: |||||| ::: |||| obeubeuvalbeuvalheuvalvalvalvalvalserbeurle 582 615 STICTICCCGGGAAACCAGGAAAAGGAICCGCIACICAAAAACCAAGAA 1723 ----TACAAAAACACAAGGAATACAAC-----:|||| ::: ::|||||||||||aProAlaSrgGlyLeuGly--

ME20 antigen (me20m) - human melanoma antigen 25

#sequence\_revision 01-Nov-1996 #text\_change 01-Dec-2000 iens (man)

; As3668; AS5753 ken, U.S.; Neubauer, M.; Aruffo, A.; Hellstrom, I.; Hellstrom, K.; Met R7-95, 1994 87-95, 1994 dexpression of the gene for the Melanoma-Associated ME20 Antigen.

iry; translated from GB/EMBL/DDBJ

IRAA

RES.

EMBL:U01874; NID:g494939; PIDN:AAA18479.1; PID:g494940

Socr. A.J.; Vogel, A.M.; Loenen, W.A.M.; Figdor, C.G.

C1164-20133, 1994

characterization of the melanocyte lineage-specific antigen gpl00.

A53668; MUID:94327568; PMID:7519602

NA 94-662 <ADE>

GB:S73003; NID:g639589; PIDN:AAC60634.1; PID:g639590 yahu, S.; Delgado, C.H.; Robbins, P.F.; Sakaguchi, K.; Appella, E.; ci. U.S.A. 91, 6458-6462, 1994

A; Title: Identification of a human melara, Reference number: A55753; MUID:9429440	f a human melanoma antigen recognized by tumor-infiltrating lym 3, MUID:94294401, PMID:8022805	ò	TAT
ence not 92,594-66	shown; not compared with conceptual translation. 2 <kaw></kaw>	op Oy	250 Tyrleualaglualaaspleuser' 935 GTTTCCACCAATCATACTGTGAAT
/coprocein		qq	:::    270 IleSerArgAlaLeuValValThr
Arignment Scores:  Fred. No.:  Score:  593.50  Percent Similarity:  39.45%	Length: 662 Matches: 167 Conservative: 93	yo du	995 CTCACTGTGAAAGCTGCAGCACCA :: ::: :::
ty: 25.34% 12,24%		ζ	1039
2 (1-2661) * T38400 (1-6	: sdi	QC	310 ThrAspGlyHisArgProThrAla
200 T		٥x	1039
		Db	330 ThrGluValValGlyThrThrPro
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AAACGATTTCATGATGTGC	CCTTCTGCTTACATGAGGGAG	qq	350 SerValGlnValProThrThrGlu
LygvalProArgAsnGinAspirpheuGiyvalSerArg		λō	1039
ACAATCAATT	AAATGGCTGGTCTTCTGATGAAAATGACTGAAAAACTCTACCCA 239	QQ	370 GluSerThrGlyMetThrProGlu
		ò	1039
GTGTGGAAGCGGGGAGACATGAGGT(	GTGTGGAAGCGGGGAGAGATGGAAAAACTCCTGGAAGGAGGCCGTGTGTGCGAGGCG 299	Ωp	390 AlaGluMetSerThrProGluAla
GluTrpThrGluAlaGlnAi		ò	1039
GTCCTGACCAGTGACTCACCAGCCCT	GTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTG 359	qq	410 LeuSerGlyThrThrAlaAlaGln
Lysvalselasimspoly <i>FloiniL</i>		δλ	1040CCACCACCAGACCTTCA
		qq	430 GluLeuProlleProGluProGlu
AGAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAAC-		δλ	1064ACCCCTTCTTTAGGACCTGCT
	lySerGlnVa	QO	IleThrGlySe
ACAGCATGGTCAGAGGACA(	-ACAGCATGGTCAGAGGACAGTGACGGGGAAAATGGCACCGGCCAAAAGCCATCAT 518	ò	1121 GAAAACTGCCAGATT :::
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AACGICTICCCIGATGGGAAACCITT	TTÇÇTCACCCCGGATGGAAGATGGAATTŢÇ 578	Š i	11/2 GIAGAGGGATCIIAGAGGIIAAC
:::		g ::	490 ValGlnGly
ATCTACGTCTTCCACACACTTGGTC	ATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGA 638	ž t	
valTyrValTrpLysThrTrpGlyG		3 8	
GTTTCTGTGAACACAGCCAATGTGA	GTTTCTGTGAACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTAC 698	<u>}</u>	
reserileglyThrGlyArgAlaM	etLeuGlyThrHisThrMetGluValThrValTyr 189	}	
AGAAGACATGGACGGGCATATG'	AGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGTACGTGGTA 755	r d	
HisArgArgGlySerArgSerTyrVa	alproLeuAlaHisSerSerSerAlaPheThrIle 209	ò	1409 ACGTACTGTGAACCTCACCTG
ACAGATCAGATTCCTGTGTTTGTGA(	ACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAGAATTCATCCGAC 815	: A	
ThraspeinvalPropheservals		δ	1469 ATTTCTGTTCTGACAGAGACCCA
GAAACCTTCCC-AAAGATCTCCCCA. :::     :::    : TweHisPhelenArdAenGlnProf.	816 GAAACCTICCC-AAAGHTCICCCCATTAIGTTTGATGTCCTGATTCATGATCCTGAGCCAC 874 ::::   -::::::    -::::::::   -:::::::	qq	::: :::    :::::: 584 LeuIleMetProGlyGlnGluAla

AGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGATC 1528 1039 1039 1039 TGGTGACAACCCCTGGAGCTGAGTAGGATTCCTGAT 1120 A------1039 -- 1039 ----- 1039 TAACAGATATGGCCACTTTCAAGCCACCATCACAATT 1171 ACATCATCCAGATGACAGACGTCCTGATGCCGGTGCCA 1231 GCTGACTGTGAGACGAACCTTC---AATGGGTCTGGG 1408 oleuThrSerCysGlySerSerProValProGlyThr 309 uLysValProValSerGluValMetGlyThrThrLeu 389 uGlyProAspAlaSerSerIleMetSerThrGluSer 449 CTTTGTCGTGACCTGCCAAGGGAGCATTCCCACGGAG 1291 CCACCTGCGAGATCACCCAGAACACAGTCTGCAGCCCT 1351 ||| ::: ::: ||I|||||| 563 | | nLeuValLeuHisGlnIleLeuLysGlyGlySerGly aGlyGly-----LeuGlyGlnValProLeuile 600 aGluAlaProAsnThrThrAlaGlyGlnValProThr 329 nValThrThrThrGluTrpValGluThrThrAlaArg 429 uLeuAspGlyThrAlaThrLeuArgLeuValLysArg 469 |||::: :::::||| ----IleGluSerAlaGluIleLeuGlnAlaValPro 503 | |||::: odlyCysGlnProProAlaGlnArgLeuCysGlnPro 543 ||||||||||:: rHisThrTyrLeuGluProGlyProValThrAlaGln 289 oGlyGlnAlaProThrAlaGluProSerGlyThrThr 349 uValileSerThrAlaProValGlnMetProThrAla 369 CTACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTT 934 TCACACGTATGTGCTCAATGGAACCTTCAGCCTTAAC 994 aThrGlyMetThrProAlaGluValSerIleValVal AAAACCC----

699 AGAAGACATGGACGGGCATATCTTCCCATCGCACAAGTGAAAGATGTACGTGGTA 755  [190 HisArgArgArgGTySerArgSerTyrValProLeualaHisSerSerSerAlaPheThrIle 209  756 ACAGATCAGATTCTGTGATTGTTCCAGAAGAACGATCGAAATTCATCCGAC 815  [          :::             :::	230 LyshiskheeuargasnGinProLeuThrPheAlaleuGlnLeuHisaspProSerGly 249 875 TTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTT 934 875 TTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTT 934 855 TYTLeualaGluAlaAspLeuSerTyrThrTrpAspPheGlyAspSerSerGlyThrLeu 269 935 GTTTCCACCAATCATAGTGATCACACGTATGTGCTCAATGGAACCTTCAGCCTTAAC 994 855 GTTTCCACCAATCATAGTGATCACACGTATGTGCTCAATGGAACCTTCAGCCTTAAC 994	270 IleSerArgAlaProvalValThrHisThrTyrLeuGluProdlyProvalThrAlaGln 289  995 CTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCGCCA 1039  ::: :::::	310 ThrAspGlyHisArgProThrAlaGluAlaProAsnThrThrAlaGlyGlnValProThr 329	330 ThrGluValValGlyThrThrProGlyGlnAlaProThrAlaGluProSerGlyThrThr 349	350 SerValGlnValProThrThrGluValIleSerThrAlaProValGlnMetProThrAla 369	1039 1039 1039 370 GluSerThrGlyMetThrProGluLysValProValSerGluValMetGlyThrThrLeu 389	1039 1039 390 AlaGluMetSerThrProGluAlaThrGlyMetThrProAlaGluValSerIleValVal 409	1039 1039 1039 1039 410 LeuSerGlyThrThrAlaAlaGlnValThrThrThrGluTrpValGluThrThrAlaArg 429	1040CCACCACCCACCACCTTCAAAACCC	1064ACCCCTTCTTTAGGACCTGCTGGTGACCACCCCTGGAGTGGTTTCCTGAT 1120	1121 GAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCACAATT 1171 :::	1172 GTAGAGGAATCTTAGAGGTTAACATCCAGATGACAGACGTCCTGATGCCGGTGCCA 1231	1232 IGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCACGGAG 1291	1292 GTCTGTACCATCATTTCTGACCCCACTGCGAGATCACCCAGAACACAGTCTGCAGCCCT 1351 
8 8 8 8 8	3 2 8 25	8 & 8 &	<u> </u>	3 8 8	<del>3</del> 8	\$ a	oy Dp	qa Dp	Qy Dp	Qy	ð 8	රු සි	Qy Dp	\$ &
Oy 1529 TCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAA 1585  Db 601 ValG1y11eLeuLeuValLeuMetAlaValValLeuAlaSerLeu11eTyrArgArg 619  RESULT 4  A41234  melanocyte-specific protein Pmel-17 precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: A41234 R;Kwon, B.S; Cfintamaneni, C; Kozak, C.A.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.; Proc. Natl. Acad. Sci. U.S.A. 88, 9228-9332, 1991	A;Title: A melanocyte-specific gene, Pmel 17, maps near the silver coat color locus on m A;Reference number: A41234; MVID:92021023; PMID:1924386 A;Accesion: A41234 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-668 <kwo> A;Cross-references: GB:M77348</kwo>	Alignment Scores:  Pred. No.: Score: Score: Score: 588.50 Matches: Percent Similarity: 39.61% Conservative: Mismatches: 170 Conservative: 93 Query Match: 12.13% Mismatches: 198 DB: 2 Gaps:			OY 126 AAACGATTTCATGATGTGCTGGGGCAATGAAAGACCTTCTGCTTACATGAGGGAG 179	Qy 180 CACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAAATGAAAAACTCTACCA 239	N	OY 300 GTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAIAIAACATTTGCGGTGAACCTG 359	OY 360 AIAITCCCTAGAIGCCAAAGGAAGAIGGCAACAIAGGCTATGAGAAGAGAGIGC 419  Db 89 AsnPheProGlySerGlnLysValLeuProAspGlyGlnVallieTrpValAsnAsnIhr 108				GAGA	

27 1352 GTGGATGTGGATGAGATGTGTCTCT	GIGGALGIGGALGAGALGIGICIGCIGACIGIGAGACCIICAAIGGGICIGG 1408	& 8	942 CCAATCATACTGTGAATCACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTG 1001 
1409	CACCCTG	<i>≿</i> 6	
1469	ATTCTGTTCCGGACAGAGCCCAGCCTTTAAGGATGCCAAACAGTGCCCTG 1525 :::	Qy Dp	1050 GA 1051 
1526		ð	1051 1051 1051 1051 1051 1051 1051
602	GlnValProLeulleValGlyIleLeuLeuValLeuMetAlaValValLeuAlaSerLeu 621	a è	10
Qy 1574 GTGTACAAAAA 1585 :::   ::::: Db 622 IleTyrArgArg 625		À A	rpValProThrThrGluAspValGlyThrThrProGluGlnValAlaThrSerLysValL 21
RESULT 5		δλ	- 10
A49179 melanoma antigen homolog rpel - bovine C.Species: Bos primigenius taurus (cati		qu .	euSerThrTh
C;Date: 19-Dec-1993 #sequence_revisic C;Accession: A49179; 145861 D:Vim D V : Wistow G J	on 18-Nov-1994 #text_change 08-Nov-1996	À qa	1052
Fixe. Eye Res. 55, 657-662, 1992 A;Title: The cDNA RPE1 and monoclonal antibody HMB-50 define gen A;Reference number: A49179; MUID:93122163; PMID:1478275	l antibody HMB-50 define gene products preferentiall 22163; PMID:1478275	ζς O	1079CCTGCTGGTGACAACC 1094 255 hrThralaGlyGluValSerThrProGluProAlaGlySerAsnThrSerSerPheMetP 275
A;Accession: A*71.73 A;Status: preliminary A;Molecule type: mRNA		δλ	
A,Residues: 1-491 «KLM» A,Experimental source: retinal pigment epithelium A,Note: sequence extracted from NCBI backbone (NCBIN:122438, NCBIP	nt epithelium backbone (NCBIN:122438, NCBIP:122439)	<b>q</b> a &	275 roThrGluGlyThrAlaGlySerLeuSerProLeuProAspAspThrAlaThrLeuVall 295
C;Genetics: A;Gene: RPE1		<b>%</b> 8	euGluLysArgGlnAlaProLeuAspCysValLeuTyrArgTyrGlySerPheSerLeuT
	Length: 491 Matches: 124 Concernsition 6	60 60	1161 CCATCACAATTGTAGAGGAATCTTAGAGGTTAACATCATCCAGATGACAGGGGGGGG
Percent Similarity: 26.67% Best Local Similarity: 26.67% Ouery Match: 2	Mismatches: 123 Indels: 155 Gaps: 14	δō :	
US-10-039-272-1 (1-2661) x A49179 (1-	(1-491)	<u>a</u> 8	
Qy 603 CAGTATTTCCAGAAATTGGGACC	CAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGGTTTCTGTGAACACAGCCAATGTG 662	දි සි	euProLysGlualaCysMetAspIleSerSerProGlyCysGlnLeuProAlaGlnArgL
663		yy Op	1341 TCTGCAGCCCTGTGGGATGTGGATGTGTCTGCTGACTGTGAACCTGTCA 1397
Db 21 MetLeuGlyThrTyrasnMetG- Qy 720 GTTCCCATCGCACAAGTGAAAG	TGTTTGTG	Qy	1398 AIGGGICIGGGACGIACIGIGAACCICACCCIGGGGAIGACACAAGCCIGGCICICA 1457
Db 41 ValProLeuAlaHisSerSerSe Qy 780 ACTATGTTCCAG	eralapheThrIleThrAspGlnValProPheSerVal 60AagaacGaTCGAAATTCATCGACGAAACC 821	νς d	1458 CGAGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCGCTTTAAGGATGGCAAACA 1517
Db 61 SerValSerGlnLeuGlnAlaLe		5	GIGCCCTGAICTCCGTIGGCTGCTTGGCCAIAITIGTCACTGIGAICTCCCTCTTGG
Qy 822 TTCCCAAAGATCTCCCCATTAT       ::: Db 80ProLeuTh	TTCCCAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCA 881	qa k	426LeuPheValGlyIleLeuLeuValLeuThrAlaLeuLeuLeuAlaSerLeuI 443
882	ATTAITCTACCATTAACTACAACTGGAGCTTCGGGGATAATACTGGCCTGTTTGTT	d Dp	443
Db 95 laGlyAlaAspLeuserlyrin	Irirpaspriiecryaspaeriiirciyiiir.muureaera 113	RESULT	9

The rich glycoprotein GAS28 precursor .hlamydomonas reinhardtii  107907  Martinez, H.; Haring, M.A.; Von Gromof the EMBL Data Library, July 1997  1070707  10707  1	Oy 1021	279 1155 299 1199	44 QY 1257 44 Db 326 548 QY 1298 57 Db 340	TCCACACACTTGGTCAGTAT 608  Protein-tyrosine-phosphatase (EC 3.1.3.48)  Protein-tyrosine-phosphatase (EC 3.1.3.48)  N.Alternate names: PTPase MEG C; Date: 20-Mar-1992 #sequence_revision 02- C; Date: 20-Mar-1992 #sequence_revision 02- C; Date: 30-Mar-1992 #sequence_revision 02- A; Ttle: Identification, cloning, and exprayable of the control of th
. UNITERATED # 4 A C # 4 H L L L L L L L L L L L L L L L L L L	28 precursor - 50 14-May-1999 7.; Von Gromof, July 1997 50 GB/EMBL/DDBJ 50 GB/EMBL/DDBJ 51 FI GBJ 52384727; PI 53 predicted <8	In glycoprotein GAS28 # Length: 446 Marches: 85 Conservative: 25 Mismatches: 123 Indels: 158 Gaps: 138	CIGGITTATCTGCT CIGGATTATCTGCT	CACCACCCGGATGG TTCCAGAAATTGGGA

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-yrosine-phosphatase (EC 3.1.3.48) PTPN4, nonreceptor type 4 [validated] - humarlete names: PTPase MEG s: Homo sapiens (man) (man) (0-May-1994 #text_change 21-Jun-2002 (0.50 AA-1105) (0.50 AA-1105)
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simily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; 18st phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphata //Domain: protein 4.1 membrane-binding domain homology <B41>
//Domain: glGF domain homology <GLGS
//Domain: protein-tyrosine-phosphatase homology <PTP>
tive site: Cys (phosphocysteine intermediate) #status predicted
nding site: Substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; York, J.D.; Warshawsky, I.; Majerus, P.W.
11. Acad. Sci. U.S.A. 88, 5867-5871, 1991
Identification, cloning, and expression of a cytosolic megakaryocyte protein-t
tee number: A41105; MUID:91288564; PMID:1648233
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                                                                                                                                                                                                    1073
                                                                                                                                                                                                                                                                                                ---GGTGACAACC 1094
                                                                                                                                                                                                                                                                                                                                                                                       1095 CCCTGGAGCTGAGGATTCCTGATGAAACTGCCAGATTAACAGATATGGCCACTTTC 1154
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                                           199 ysTyrThrSerArgLeuPheAsnGlnAspArgAspCysCysProValSerIleLeuGlyA 219
                                                                                                                                                                                                                      239 roProProSerProProProProProProProThrProSerProProProGluL 259
                                                                                                                                            219 snAlaProProProHisValProSerProSerProProSerProSerProSerPro 239
                                                                                                                                                                                                                                                                                                                                    259 eubroProAlaGlnProAspAlaProAlaArgLysArgProProProProAlaSerPro† 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 -------CysGluAsn-----ProAsnSerLysCysCluPheGluLeuTyrL 340
                                                                                                                                                                                            le type: mRNA
ss: 1-926 <GUA>
references: GB:M68941; NID:g190747; PIDN:AAA36530.1; PID:g190748
mental source: megakaryocytes, cell line MEG-10.
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127
141
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Mismatches:
Indels:
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Matches:
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129.00
32.41%
22.03%
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1021
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Mon

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apolipoprotein(a) - western Buropean hedgehog (fragment)
C;Species: Brinaceus europaeus (western Buropean hedgehog)
C;Species: Doct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C;Accession: T18518
R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong A; Biol. Chem. 270, 24004-24009, 1995.
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot A;Reference number: 146259; MUID:96025778; PMID:7592597
A;Accession: T18518
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Residues: 1-2869 <LAW>
A)Cross-references: BMBL:U33170; NID:g1046358; PID:g1046359; PIDN:AAC48522.1
A)Experimental source: liver
C)Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con
------CCTTCAAAACCCACCCTTCTTAGGACCTGCTGGTGACAACCCCCTGGAG 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGAT 386
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                                            517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||| ::: |||::: |||||||||| oproThrGluProMetVal-ValProGlyGln------CysLeuGluGlyThrG
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                          1103 CTGAGTAGGATTCCTGATGAAACTGCCAGATTAACAGATATGGC 1147
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--GlyArgPheGly 529
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Matches:
Conservative:
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                                                                                                                             518 IleArgMetLysProAspGluAsn---
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Best Local Similarity:
Query Match:
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Pred. No.:
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Db 844 isThrCysGl Qy 1406	Db 864 yrProThrLy	1439	883	1485	DD 903 IUSErProTh	Db 923 GlyGluAsnT	Oy 1554		1555	962		787	Qy 1665 CAAAGCCGT ::: Db 1002 rGlubroMet	RESULT 9 S21766	dihydrolipoamide S-acety C.Species: Rattus norveg	C; Date: 22-Nov-1993 #seq	A:Title: Molecular cloni	A, Reference number: S217/	A)Accession: S21/66 A)Molecule type: mRNA A:Residue: 1=cc /www.	A;Experimental source: h	A;Genome: nuclear C;Complex: component E2	C;Function: A;Description: catalyzes	A,Pathway: pyruvate metal C,Superfamily: dihydroli	C; Keywords: acetyl-CoA; E:7-81/Domain: lipoyl/bic	F;133-207/Domain: lipoyl, F;254-307/Domain: compone F;46,172/Binding site: li	F;528,532/Active site: Hi	Pred. No.: Score:	Percent Similarity: Best Local Similarity:	Query Match: DB:	US-10-039-272-1 (1-2661)
441 GCTGATCCATATGTTTACAACTGGACAGCATCGTCAGAGGACAGTGACGGGGAAAAT 497				618 TIGGGACGAIGTICAGIGAGGTITCTGIGAACACAGCCAAIGIGACACTIGGGCCTCAA 677		678 CTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATC 728        ::     634 alvalproglyGlnCysLeuGluGlyThrGlyGluAsnTyrArgGlySerValAlavalT 654		 654 hrValSerGluHisThrCysGlnArgTrpArgGluGlnSerProHisSerHisSerTrpT 674	786 ITCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCATTATGT 845	674 hrProglu 676	846 TIGAIGICCIGAITCAIGAICCIAGCCACTICCICAATTAITCIACCAITAACIACAAGI 905	677	906 GGAGCTICGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATA 950 ::::::		705 laValArgTrpGluTyrCyss 712	1011 CAGCACCAGGACCTTGTCCGCCACCGCCACCACCCAGACCTTCAAAACCCACCC		1071 CTTTAGGACCTGCTGGTGACAAC			1128 GCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAG 1187	772 roThrLysAsnLeuValGlyAsnTyrCysArgAsn 783	1188 AGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCC 1247	784	1248 TAATAGACTTGTGGACCTGCCAAGGAGGATTCCCACGAGGGTCTGTACCATCATT 1307 788 1=1307			1368 IGTGTCTGCTGACTGTGAGGACGAACCTTCAATGGGTCT1405	824 lnCysLeuGluGlyThrGlyGluAsnTyrArgGlySerValAlaValThrValSerGlyH 844	1405 1405
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kano, K.; Ohta, S.; Shimura, M.; Yamanaka, T.; Nakagawa, S.; Titani, K.;
. Acta 1131, 114-118, 1992
ar cloning of dihydrolipoamide acetyltransferase of the rat pyruvate deb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ate metabolism hibydrolipoamide acetyltransferase; lipoyl/biotin-binding homology lihydrolipoamide acetyltransferase; cardiac muscle; coenzyme A; heart; lipoamide; rapoyl/biotin-binding homology <LPB1>
11 lipoyl/biotin-binding homology <LPB2>
12 component E3 binding #status predicted <E3B>
13 site: lipoamide (Lys) (covalent) #status predicted : site: lis, Asp #status predicted
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                                                -------GGACGTACTGTGTGAACCTCACCTGGGGGAT----- 1438
                                                                                                                                                      -----GACACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGAC---A 1484
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                                                                                                                                                                                         TrpCysTyrThrThrAsnSerAlaValArgTrpGluTyrCysSerIleProAlaCysG 903
                                                                                                                                                                                                                                                                                                    SerProThrProProThrGluGln-GlnValValProAspGlnCysLeuGluGlyThr 922
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ThrCysGlnArgTrpArgGluGlnSerProHisSerHisSerTrpThrProGluAsnT 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-acetyltransferase (EC 2.3.1.12) - rat (fragment) s norvegicus (Norway rat)

993 #sequence_revision 01-Feb-1999 #text_change 05-May-2000
                                                                                                                                                                                                                                                         GACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTG------
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luProMetValValProGlyGlnCysLeuGluGlyThr 1015
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ource: heart
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1-2661) x S21766 (1-555)

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1619
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ATCACACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCAC 1016
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hrvallleArgGlnAsnHisValValAspValSerValAlaValSerThrProAlaGlyL
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213 IlealaAlaPheAlaAspTyxArgProThrGluValThrSerLeu--LysProGlnAlaP
                                                                            1107 GTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA
                                                                                                                                                                                                                                     CAATTGTAGAGGA---ATCTTAGAGGTTAACATCATCAGATGACAGACGTCCTGATGC
                                                                                                                                                                                                                                                                                                                                                                                                               1293 TCTGTACCATCATTTCTGACCCCACCTGCGAGATCACCCCAGAACACAGTCTGCAGCCCT-
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                                                                                                                    CCCCTTCTTTAGGACCTGCTGGTGAC--
                                                              CAGGACCTTGTCCGCCACCG-
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surface protein type 51B - Paramecium tetraurelia C;Species: Paramecium tetraurelia

RESULT 10

in Paramecium tetraure C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 07-Dec-1999 C;Accession: S50820
R;Scott, J.; Leeck, C.; Forney, J.
Nucleic Acids Res. 22, 5079-5084, 1994
A;Title: Analysis of the micronuclear B type surface protein gene in Paramecium tet A;Reference number: S50820; MUID: 95098630; PMID: 7800503
A;Accession: S50820
A;Accession: S50820
A;Accession: S50820
A;Accession: J.2395 ScOD
A;Accession: J.2395 ScOD
A;Accession: J.2395 ScOD
A;Accession: J.2395 ScOD
A;Coss-references: EMBL: U07603; NID: 9467226; PIDN: AAA81947.1; PID: 94467227
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
C;Genetics
A;Genetics
A;Genetics
A;Genetics
C;Genetics
C;Genetics
C;Coperfamily: G surface protein 1359 1414 erThrCysValTyrAlaValGluGlyGluCysValValSerGlyThrSerCysValArgL 1434 ::::::: ||| eAlaLeuGlyThrSer-GlyCysGlnThrLysThrCysAlaAsnLysThrThrProPheA 1379 ::: |1304 ThrThrIleAlaAsnCysTyrArgSerThrAla-GlyTyrCysThrAlaAsnSerGlyAs 1323 pserAlaCysGlnAlaileSerAlaSerThrThrCysGluGlnIleLysLeuGlySerSe 1343 830 875 632 692 737 775 TCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAAT 497 GGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATA 341 Ľ--------TGTGACTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAG 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 07-Dec-1999 AAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTA ATGGGAAACCT TITCCTCACCACCCCGGATGGAAGATGGAATTTCATCTACGTCTTCCACACACTTGGT ---ACGATGTTCA GTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAGTGACT 693 GTCTACAGAAG-----ACAIGGACGGGCATAIGITCCCAICGCACAAGIG LysArgAspGlyThrGlyCysValThrIleGlnSerAlaCys----831 ATCTCCCCATTATGTTTGATGTCCTGATTCATGATCCTAGCCAC-2395 107 48 165 182 28 Length:
Matches:
Conservative:
Mismatches: GGCACCGGCCAAAGCCATCATAACGTCTTCCCTG---ACATTTGCGGTGAACCTGATATTCCCTAGATGCCAA-434 ysThrCysAspThrAlaSerAlaAspThrSer-AAAGATGTGTACGTGGTAACAGATCAGAT----Indels: US-10-039-272-1 (1-2661) x S50820 (1-2395) 603 CAGTATTTCCAGAAATTGGG-----0.344 114.00 30.88% 21.31% 2.35% :: 1379 la-----Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: 738 1323 1359 1287 438 498 543 633 282 342 378 1343 Query Match: DB: Db Db a à g ò QD ð g ò g à 8 ⋩ à g à g ð 8 g δ

A; Experimental source: strain MHOM/IL/81/Friedlin C; Genetics: A; Gene: L4171.3 A; Map position: 1 Alignment Scores: Pred. No.: Pred. No.: 113.00 Matches: Percent Similarity: 37.588 Mismatches: 60 Query Match: 2.338 Mismatches: 60 Query Match: 2.338 Mismatches: 60 DB: 2.338 Mismatches: 60 Gaps: 6	US-10-039-272-1 (1-2661) x T02831 (1-1541)  QY 1022 CCTTGTCCGCCACCCACCCACCCAGACCTTCAAAACCCACCC	Oy 1433 GGGATGACACAGGCTCTCACGAGCACCTGATTTCTGTTCTGACACACAC	70 kd mitocl
Db 1445		1620 eug 1371 GTC 1638 Ys 1428 CCC 1652 hrG] 1652 hrG] 1672 sp 1	RESGUE 11  AAA Protein 14171.3 [imported] - Leishmania major (strain Friedlin)  C; Species: Leishmania major C; Species: Leishmania major C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000 C; Accession: C81460; T02831 R; Myler, P.J; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; A; Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-chanders: A81455; MuID:99178987; PMID:10077609 A; Accession: C81460 A; C81460

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A)Status: preliminary
A)Molecule type: DNA
A)ROJecule type: DNA
A)ROJecule type: DNA
A)ROJecule type: NA
A
C;Accession: C81466; T02831
R;Myler, P.U.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
A;Reference number: A81455; MUID:99178987; PMID:10077609
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1022 CCTIGICCGCCACCACCACCACCACCAGACCTICAAAACCCACCCTICITIAGGACCT 1081
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Matches:
Conservative:
Mismatches:
Indels:
perimental source: strain MHOM/IL/81/Friedlin
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hrVallleArgGlnAsnHisValValAspValSerValAlaValSerThrProAlaGlyL 344
                                                                                                                                                                                                                                                                                                                      167
A,Pathway: pyruvate metabolism
C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homol
C;Reywords: acetyl-CoA; acyltransferase; coenzyme A, lipoamide; mitochondrion
F;48-122/Domain: lipoyl/biotin-binding homology LPB2>
F;169-222/Domain: component E3 binding #status predicted cE3B>
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364 alValSerLeuAlaSerLysAlaArgGluGlyLyByEeuGlnProHisGluPheGlnGlyG
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|I|eAlaAlaPheAlaAspTyrArgProThrGluValThrSerLeu--LysProGlnAlaP
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187 ysLeuAlaAlaGluLysGlyIleAspLeuThr------
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2946 <DUZ>
A;Cross-references: EMBL:U40410; NID:g1065453; PID:g1065455; PIDN:AAA81392.1; CESP:C54G
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46/1; 2561/2; 2603/2; 2626/2; 2665/2; 2716/3; 2804/3; 2884/3
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|| ThrSerAsnGlnCysPheAspGluSerGluCysValPheGlyIleCysThrCysTrhrGly
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                                                                                                                spAsnGluLysGly 428
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DB:	1827 GGILAGAAGGCTIGAGIGICITTICICAACGGIGCAAAAGCCGTGTTCTTCCCGGG 1686	ζ.
Percent Similarity: 29.9 Best Local Similarity: 25.9		qa
Alignment Scores: Pred. No.: 0.4	1556 1567 CCTCTTGGTGTACAAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGT 1626	70
F;78-89,105-126,218-241/Dis	GAIGGCAAACAGIGCCCIIGAICICCGIIGGCTGGCTIGGCGAIATITGICACIGIGAICIC 15	3 8
F;351-497/Region: proline-r F;63,125,344,345/Binding si	theuricheurigemineluvalelyelmaspseraspelulysaspserfeluserleu 1 GATGCCbbbCbgTGCCTGCATGATGCCATTGATGATGATGATGATGATGATGATGATGATGATGATG	} &
F;276-321/Region: proline-rr F;348-437/Region: histidine	1447 CUIGGUTUTCACGAGCACCTGATTTCTGACAGAGAGCCGAGCC	λ d
F;19-131/Domain: cystatin h F:140-246/Domain: cystatin h	_	an o
C; Keywords: duplication; gl		ζλ
A;Map position: 3q27-3q27 C;Superfamily: histidine-ri	1501 nGlyGluValCysIleAsnGlySerValCysGlyAspSerAsnCysGluCysThrGl 1520	qq
A;Gene: GDB:HRG A;Cross-references: GDB:120	1327 CACCCAGAACACAGICIGCAGCCCIGIGGAIGIGGAIGAGAIGIGICIGCIGACIGIGAG 1386	δy
e-rich' region. C;Genetics:	1481 yLysArgLeulleLeuGlyIleCysValPhelleAlaLeuProGluThrSerCysGluAs 1501	qq
ould not have inhibitory ac	1279 CAITCCCACGGAGGTCTGTACCATTTCTGACCCCACCTGCGAGAT 1326	Οy
lood coagulation cascade. C;Comment: The amino half o	1461 uAspSerMetCysLeuSerGlySerGluCysValAspGlyLysCysLeuCysSerAspGl 1481	qq
C;Comment: Although its phy din, and the lysine-binding	1232TGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAG 1278	Qy
A;Residues: 214-247 <hen> A;Cross-references: EMBL;Zl</hen>	1441 yAsnCysVallleValGluAspSerTyrAspLeuThrProlleAspGlyAsnCysAspGl 1461	qu
A;Status: preliminary A;Molecule type: DNA	1193 -AACATCAGATGACAGACGTCCTGATGCGGTGCCA 1231	Οy
A;Reference number: S29669 A;Accession: S29669	1421 nSerileLeuGlyLeuGlyArgileCysGlnCysValGluAsnThrValLeuTrpAsnGl 1441	ΩĐ
submitted to the EMBL Data A, Description: PCR detection	1168 AATTGTAGAGGGAATCTTAGAGGTT1192	ζ
A;Cross-references: GB:AB00 R;Hennis, B.; Havelaar, A.;	:::	qq
A; Molecule type: mRNA A; Residues: 1-525 < KOI>	1108 TAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACATCAC 1167	λō
A, Reference number: A01287, A, Accession: A01287	   nProLeuGlyLysGluPheArgPheSerGluGlyLysLysIleGluMetArgArgThrSe	qa
Biochemistry 25, 2220-2225, A;Title: Amino acid segment	(1)	ΟŊ
C;Accession: A01287; S29669 R;Koide, T.; Foster, D.; Yo		qa
C;Species: Homo sapiens (ma C;Date: 04-Dec-1986 #sequer	1033 ACCGCCACCACCACCAGACCTTCAAAACCCACCCTTTTAGGACCTGGTGACAA 1092	λŏ
histidine-rich glycoprotein N,Alternate names: HRG	1350 sGluAsnGlnPheCysArgCysLeuGlnAspValAlaAlaGluAsnGlylleCysProPr 1370	qa
RESULT 14 KGHUGH	973 CAAIGGAACCTICAGCCITAACCICAGAAAGCIGCAGCACCAGGACCTIGICGGC 1032	ζ
Db 1636LysAsp	1333 eProGlyGluTyrCysGlyThrGlyGlnValCysLeuGlyAsnSerValCy 1350	qa
Qy 1816 TTTCCTAAAGAT	913 GGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATCACACGTATGTGCT 972	Qy
Db 1621 yCysSerGluThr	1313 rGlyAlaLysThrValAlaGluGluGluAsnAsnSerThrMetLysTyrLysIleAlaPh 1333	DÞ
Qy 1766ACT	881	ζö
Db 1601 ThrGluAsnCys		qa
Oy 1747 GACC	866	δ
Db 1581 nAspGlnGluCys		qq
Oy 1687 AAACCAGGAAAAC	856 GATTCATGAT 865	QY
Db 1569 uValArgArgGlu	1253 oLeuGlnAsnThrLeuLysAsnGluPheArgGlyLeuGlnGluIleSerAsnAspGlyLe 1273	qa
	838 CATTATGTTTGATGTTTGATGTTTGATGTTTGATGTTTGATGTTTGATGTTTGATGTTTGATGTTTGATGTTTGATGTTTGATGTTTGATGTTTGATGTTTTGATGTTTTGATGTTTTGATGTTTTGATGTTTTGATGTTTTGATGTTTTTT	ò

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of this protein is homologous to the first two cystatin-like (ctivity. having a high histidine and proline content, this protein has
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.; Kluft, C.
a Library, October 1991
ion of a dinucleotide repeat in the human histidine-rich glyco
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ace of human histidine-rich glycoprotein derived from the nucl
7; MUID:86216149; PMID:3011081
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	Description	BC025297 Homo sapi AK044764 Mus muscu AK076347 Mus muscu BX397314 BX397314
SUMMARIES	ID	2636 11 BCC25297 3615 11 AKO44764 2265 11 AKO76347 1201 13 BX397314
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    info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvanek Sasedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TWAGE:4877773"
/clone="TWAGE:4877773"
/clone="Tibe="NIH MGC 49"
/clone libe="NIH MGC 49"
/lab_host="DH10B-R"
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Best Local Similarity 99.1
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Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Furuno, M., Hanagaki, T., Hara, A., Habhizume, W., M., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Kawai, J., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Sato, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/
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                                          I & II Team.
the mouse transcriptome based on functional annotation
ill-length cDNAs
                                                                                                                                                                                                                                                                   Carninci, P.,
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CDM library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
onsortium and the RIKEN Genome Exploration Research
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AKO44764

AKO44764

Mus musculus adult retina cDNA, RIKEN full-length enriched library, clones.A930040L12 product:glycoprotein (transmembrane) nmb, full insert sequence.

AKO44764

AKO44764.1 GI:26336782

HTC; CAP trapper.

RESULT 2
AK044764
LOCUS
DEFINITION

ACCESSION VERSION KEYWORDS

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GACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGC
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                                                                                                                                                                                                                                  /tissue_type="retina"
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100._1824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATGCC
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(transmembrane) nmb (MGD|MGI:1934765, GB|NM_053110,
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                                                                                                                                                                                                                                                                                                                                                                        evidence: BLASTN, 99%, match=2272
                                                               /organism="Mus musculus"
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/db_xxef="MG1:2410100"
/db_xxef="taxon:10090"
/clone="A930040L12"
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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3600. .3605
/note="putative"
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/note="putative"
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Best Local Simil
Matches 1409; C
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S. Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Hayatsu, M., Hangaki, T., Hiraoka, T., Hirozane, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imorani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matanyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Salto, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (16-ARP-2002) Yoshinide Hayashizaki, The Institute of Submitted (16-ARP-2002) Yoshinide Hayashizaki, The Institute of Submitted (16-ARP-2002) Wilking Seearch (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Wanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9222, Fax:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTAINST ALTONE MESTICOYLOFILLANGIPLODARKERDVIGHEQYPDHMREHNQL
RGWSSDENEWDEHLYPVWRRGDGRWKDSWEGGRVQAVLTSDSPALVGSNITFVVNIVP
RCQKEDANGINIYERKORRNJGLTSDLHVYNWTAGADDGDWBEDGTSRSGHLRFEPBRR
PEPRPHGWKKWSTVYVFHTLGQYFQKLGRCSARVSINTVNLTAGPQVMBVTYFRRYGR
AYIPISKVKDVYVITOQIPVFVYMSQKNDRNISDEIFRADLEYVFDVLHIDPSHFLND
SALSYKNNFGDWTGLFVSNNHTLNHTYVLNGTFNLNLTVQTAVPGPCPPSFSTPPPP
STPPSPPPSPPPSPLSTPSPSLMFTGKSMELSDISMRKRINKYGYFRATITIVEGTL
BVSIMQLADVPWFTPQPANSLMDFTVTCKGATPBMEATIISDFTCQIAQNRVCSPVAV
DGLCLLSVRRAFNGSGTYCVNFTLGDDASLALTSTLISIPGKDDDSPLRANNGVLISI
GCLLAVLYTWYTILLYKKHKAYKPIGNCPRNTVKGKGLSVLLSHAKAPFFRGDGEKDPL
                         Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
(bases 1 to 2265)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Gaps
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(transmembrane) nmb (MGD|MGI:1934765, GB|NM_053110,
evidence: BLASTN, 99%, match=2272)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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73.9%; Pred. No. 1.9e-159;
Live 0; Mismatches 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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/db_xref="FANTOM_DB:4732452017"
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/db_xref="taxon:10090"
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/note="putative"
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/note="putative"
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Best Local Similarity 73.9
Matches 1407; Conservative
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JOURNAL
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1541 TIGGCCATATITGTCACTGTGATCTCCCTCTTGGTGTACAAAAAACACAAGGAATACAAC 1600
                                                                                                                                                                                             1690 CCAATAGGAAACTGCCCCAGGAACACGGTCGAGGGCAAAGGCCTGAGTGTTCTCCTCAGC 1749
                                                                                                                                                                                                                                                                        CGTGCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAA 1720
                                                                                                                                                                                                                                                                                                                                            1781 TGATGTGAGATGTGCTGGA----GTGGCTATTAACCTTTTTTCCTAAAGATTATTGTTA 1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1869 GTATGTGAGCTGTGCAGAAGTATGTGGCTAGCTGTTGTTGTTCTCTAAGGATTATTGTAA 1928
                                                                                                                                                                                                                                                                                                                                                                                                                                     1780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK076347

2265 bp mRNA linear HTC 18-SEP-2003

Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
Library, clone:4732452017 product:glycoprotein (transmembrane) nmb,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Sonno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiwi, M., Yondeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence nonlysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Czaniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                1630 cridectricricaccarderracearctricereracaaaaaacacaadeecaracaa
                                                                                                                                    CCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1810 CCÁAGGÁCÁCTCTAAGTCÍTTGGCCTTCCCÍCTGACCAGGAACCCÁCTCÍTCTGÍG-CAÍ
                                                                                                                                                                                                                                                                                                                                                                                                                1721 GAATITAAAGGAGTITCTTAAATTICGACCTIGITTCIGAAGCTCACTTTTCAGIGCCAT
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The FANTOM Consortium and the RIKEN Genome Exploration Research
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cgj.bin/cluster.cgi?seq=CSODI033CC03NPl&cluster=4396.f. Contact
Feng Liang Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI033CC03NPI.
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                  BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4396.f.
more information about this cluster, see
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BX379978 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI042XI21 3-PRIME, mRNA sequence.
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/mol_type="mRNA"

/mol_type="mRNA"

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/dow_refe="taxon:9606"

/clone="CSODIOLAYIZ1"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="Ist strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and ECOR V

sites of the pCMVSPORT 6 vector. Library was normalized."
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Catarrhini; Hominidae; Homo.
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BP 191 91006 EVRY cedex - France
Bmall: Seqrefegenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4396.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI042AEIINP1&cluster=4396.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI042AEIINPI.
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Eukaryota, Metazoa, Chordata, Craniata, Verte
Mamaalia, Eutheria, Primates, Catarrhini, Hon
(bases 1 to 1052)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Unpublished (2001)
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AL Nature 420, 563-573 (2002)

E Gonome 420, 663-573 (2002)

E Gonome 420, Fr. Hayarsu, M., Harando, M., Harando, M., Harando, M., Harando, M., Kadando, M., Kadando, F., Imotani, K., Ishiia, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kavata, I., Kawata, M., Kojima, Y., Itoh, M., Mazaki, M., Muranda, M., Ohaca, M., Okazaki, M., Ohno, M., Ohacho, M., Okazaki, D., Shibata, K., Sahibata, K., Sahibata, K., Sahibata, M., Sakai, C., Sakai, K., Takando, H., Takando, H., Takando, H., Takando, H., Takando, M., Tak
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Physical and Chemical Research (RIKEN), Laboratory for Genome
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AK079220 Mus musculus adult male urinary bladder CDNA, RIKEN full-length enriched library, clone:9530038P20 product:glycoprotein
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                          (transmembrane) nmb, full insert sequence.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AYIPIGKVKDVYVITDQIPVFYTMSQKQDRNLSDEIFLRDLFIVFDVLIHDESHFLND
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DGLCLLSVRRAFNGSGTYCVNFTLGDDASLALFSTLISIPGKDPDSPLRAVNGVLISI
                                                                                                                     CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/.
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PRCQKEDANGNIVYEKNCRNDLGLTSDLHVYNWTAGADDGDWEDGTSRSQHLRFPDRR
                                             Yokohama
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RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yo Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, VKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product; glycoprotein (transmembrane) nmb (MGD|MGI:1934765, GB|NM_053110, evidence: BLASIN, 99%, match=2272)
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Pred. No. 6.9e-143;
0; Mismatches 337;
                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
/db.xref="FANTON D8:9530038P20"
/db.xref="MG1:2399691"
/db.xref="taxon:10090"
/clone="9530038P20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="urinary bladder"
/clome lib="RIKEN full-length
/dev_stage="adult"
48. .1628
                                                                                                                                                                                                                                                                                                                                                'organism="Mus musculus"
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/db_xref="GI:26347859"
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                                                                                 CATGTCTACAACTGGACTGCAGGGGAGATGATGGTGACTGGGAAGATGGCACCAGCCGA
                                                                                                           AGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAAGA
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BX458448 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE003Y118 3-PRIME, mRNA sequence.
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1 (Dases 1 to 1015)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                      ATAGATATTGTGGTTTTGGGGAAGTTGAATTTTTTTATAGGTTAAATGTCATTTTAGAGATG
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CATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAGATTATTGTTAA
                                824 CATTGATGTGAGAGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAGATATTATTGTTAA
                                                                                                                                                    GGGAGAGAGGATTATACTGCAGGCAGCTTCAGCCATGTTGTAAAACTGATAAAAACTT
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/mol_type="mRNA"
/db="mRNA"
/db= taxon:9606"
/clone="CSODNYO04X18"
/dev stage="Adult"
/clone lib="Homo sapiens ADULT BRAIN"
/clone lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6
/cloned into the Not I and EccRV sites of the pCMVSPORT 6
/vector. Library was not normalized."
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Introden. This sequence belongs to sequence cluster 4396.f For more information about this cluster, see
more information about this cluster, see
more information about this cluster, see
for information about this cluster, see
for information about this cluster, see
for information about this cluster, see
http://fulllength.invitrogen.com/InvitroGen.com/France
Faraday Avenue Genoscope sequence ID : CSODNO04BA09NP1.
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                                                                                                                  GECAAAGACCCAGACTCCCTCTGAGAGCAGTGAATGGTGTCCTGATCTCCATCGGCTGC 1577
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1 (bases 1 to 1003)

1 (bases 1 to 1003)

1 (bases 1 to 1003)

1 (bases 2 to 1003)

1 (bases 3 to 1003)

1 (bases 4 to 1003)

1 (bases 6 to 1003)

1 (bases 6 to 1003)

1 (bases 6 to 1003)
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                                GACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGC
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BX423077.1 GI:30766236
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       ACACTCATGAACTCCTGATGGAACAATAACAGGCCCAAGCCTGTGGTATGATGTGCACAC 356
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1139)
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqretégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4396.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AN005CE05Opl&cluster=4396.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://tulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOAN005CE05QPl.
                                                                                                                                                                                                                                            2376 AGTTAGTGCTTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGTGTATATTTCCAA
                                                      2316 TACTITGCTTGGCTGAGGGAATGATATTCATATTTCATTTTATTCCATGGACATTT
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                                                                                                                                                                                             295 TACTITGCTTGGCTGAGGGAATGATATTCATATATTCATTTATTCCATGGACATT
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Pred. No. 1.1e-138;
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/db_xref="taxon:9606"
/clone="CS0DN005xJ09"
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/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: sequen6scope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4396.f For
more information about this cluster, see
                                                                                                                                                           http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODE003BE09NPl&cluster=4396.f. Contact
egi-bin/cluster.cgi?seq=CSODE003BE09NPl&cluster=4396.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODE003BE09NPl.
Location/Qualifiers
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|db xref="taxon:9606"
|clone="CS0DE003Y118"
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1 (bases 1 to 1201)

2 ii, W.B., Gruber, C., Jessee, J. and Polayes, D.

Rull-length cDNA libraries and normalization

3 Contact: Genoscope

4 Contact: Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Bmail: seqret@agenoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 4396.f For

http://www.genoscope.cns.fr/ogi-bin/cluster.gi?seq=CSODI033CC03QPI

&cluster=4396.f. Contact: Feng Liang Email: fliang@lifetech.com

Faraday Avenue Genoscope.com/ InvitroGen Corporation 1600

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clone CSODI033YP05 5-PRIME, mRNA sequence.
EX336884
TCTGCAGCCCTGTGGATGTGGATGAGTGTCTGCTGACTGTGAGACGAACCTTCAATG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI033YF05"
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162 147 222 207 282 267 342 327 402 387 447 522 507 582 567 1002 462 642 822 87 627 702 687 747 762 807 998 926 /tissue\_type="PLACENTA COT 25-NORMALIZED"
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized. 882 942 Accrigasidecreceredadarreascareaarerereraciarirecressir TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG rrcrecricerdechadarreccaerrangedecededaacdarrrcardarerecres AACCITIGGTGCCTGCGTCCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGAGACATGAGGTGGA AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG TGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG CCAATGGCAACATAGTCTATGAGAAGTACTGCAGAAATGAGGCTGGTTTATCTGCTGATC CATATGTTTACAACTGGACAGCATGGTCAGAGGACAGAGAGGGGAAAAATGGCACCGGCC ccaaigecaacaiagiciaigagaagaacigcagaaigageciggiiiaicigcigaic AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA GATGGAATTTCATCTACGTCTTCCACACTTGGTCAGTATTTCCAGAATTGGGACGAT GTTCAGTGAGGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG 763 TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT Gaps GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT CATCCGACGAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC 867 CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT CATCCGACGAAACCTTCCTCAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC Length 1201; 5; Indels Score 910.6; DB 13; Pred. No. 2.2e-137; 2 Mismatches

573 567 633 627 693 687 753 747 813 807

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1012 bp mRNA linear EST 22-WAY-2003 BX458449 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE003YI18 5-PRIME, mRNA sequence.
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Homo sapiens
Homo sapiens
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cobra libraries and normalization
Umpublished (2001)
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                                                                              CATATGITTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAATGGCACCGGCC
                                                                                                                                                    AAAGCCATCATAAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA
                                                                                                                                                                          GTTCAGTGAGAGTTTCTGTGAACACACCAATGTGACACTTGGGCCTCAACTCATGGAAG
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                                     454 CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC
                                                                                                                 GATGGAATTTCATCTACGTCTTCCACACTTGGTCAGTATTTCCAGAAATTGGGACGAT
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BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4396.f |
more information about this cluster, see
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BX458449.1 GI:31025019
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@qenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4396.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1A1006ZG04QPl&cluster=4396.f. Contact:
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS1A1006ZG04QPl.
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                                                                                                           O mRNA linear EST 05-MAY-2003
COT 25-NORMALIZED Homo sapiens cDNA
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1. (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cobra libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCTTGGTGCCTGCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT
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1201 bp mRNA
BX364871 Homo sapiens PLACENTA COT 25-NORN
clone CSODI024YA06 5-PRIME, mRNA sequence.
BX364871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1024YA06"
                                                                                                                                                                                          BX364871.1 GI:30380860
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Homo sapiens
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1138 bp mRNA linear EST 15-MAY-2003
BX406948 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
ES0DN005YJ09 3-PRIME, mRNA sequence.
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/tissue_type="ADULT BRAIN"
/dev_stage='adult"
/clone_lib='Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Brail: 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4396.f For
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSOAN005CE05NPl&cluster=4396.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen.Corporation 1600
                                                                                                                                        CATCCGACGAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC
                                                                                                                                                                                                                       CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG
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Location/Qualifiers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
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No. 1.7e-130;
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/mol_type="mRNA"
/db xref="taxon:9606"
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                                                                                                                                                                              /organisa="Homo sapiens"
/mcl_type="mRXM"
/mcl_type="mRXM"
/db_xref="taxon:9606"
/clone="cSOBEON3YI18"
/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens"
/clone_T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 ACCTIGAGIGCCTGCGTGAGAATTCAGCATGGAATGTCTCTACTACTATTTCCTGGGAT 166
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http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?eeq=CSODE003BE09QPl&cluster=4396.f. Contact
cgi-bin/cluster.cgi?eeq=CSODE003BE09QPl&cluster=4396.f. Contact
Feng Liang Email : fliangalifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODE003BE09QPl.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection
Umpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
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llarity 99.7%; Pred. No. 2.4e-130;
Conservative 0; Mismatches 1;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:30529955"
/lab host="DH10B-TonA (T1 and T5 phage resistant)"
/clone="Organ: Pooled muscle (cardiac and skeletal);
/vector: pGWV-SPORT6.1; Site 1: ECORV (destroyed); Site 2:
Vector: pGWV-sport6.1) Site 1: ECORV (destroyed); Site 2:
Vector: pcWV-sport6.1) Site 2: ECORV (destroyed); Site 2:
Vector: pcWV-sport6.1) Site 2: ECORV (destroyed); Site 3: ECORV (destroyed); Site 2: ECORV (destroyed); 300 360 829 889 120 949 180 9 National Cancer Institute / NIH
Bldg. 31 RmloA07 Bethesda, MD 20892
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. Wichael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: WGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAMG18 row: f column: 12
High quality sequence stop: 719. 481 ATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCACGGAGGTCTGTACCATCATTCT ACTGTGAATCACACGTATGTGCTCAATGGAACCTTCAGCTTAACCTCACTGTGAAAGCT CAGATTAACAGATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAG cagaitaacagatateeccacttrcaaeccaccatcacaattetagagggaatcttagag GTTAACATCATCCAGATGACAGACGTCCTGATGCCGGTGCCCATGGCCTGAAAGCTCCCTA GITAACAICAICCAGAIGACACGACCIGAIGCCGGTGCCAIGGCCTGAAAGCTCCCTA GATCTCCCCATTATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCT GCAGCACCAGGACCTTGTCCGCCACCGCCACCACCCAGACCTTCAAAACCCACCT retritaggacergergatgacaaceceerggagergagraggarreergargaaaaerge GTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCC-CAAA 1 GIGITIGIGACIAIGITCCAGAAGAACGATCGAAATICAICCGACGAAACCTTCCICAAA TCTTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGAGTAGGATTCCTGATGAAAACTGC 61 GATCTCCCCATTATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCT þe Gaps 2; Length 895. 1310 à

841 ATTAGTCCTGGGAATGTGGTCAGAAAGGCCCTGAGTCTCTTTCTCAACC 893	qq
1610 AATAGTCCTGGGAATGTGGTCAGAAGG-CCTGAGTGTCTTTCTCAACC 1661	δ
 781 TITGICACTGTGATCTCCCTCTTGGTGTACAAAAAACACAAGGAATACAACCCAATAGAA 840	අු
1550 ITTGTCACTGTGATCTCCCTCTTGGTGTAAAAAACACACAAGGAATACAACCCAATAGAA 1609	λο
721 CCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGGC	qa
 1490 CCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGGC	δλ
661 CIGGGGGAIGACACAAGCCIGGCICTCACGAGCACCCIGALTICIGIICCIGACAGAGAC 720	Db
 1430 CIGGGGATGACACACAGCTGGCTCTCACGAGCACCTGATTTCTGTTCCTGACAGAGAC 1489	δ
 601 TGTCTGTGACTGTGACGACGAACCTTCAATGGGACGTACTGTGAACTCACGACGACGACGAACTCACC 660	qq
 1370 TGTCTGCTGAGAGAGAGACTTCAATGGGTCTGGGACGTACTGTGAACCTCACC 1429	δλ
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Search completed: September 10, 2004, 09:57:44 Job time : 10044 secs

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Q96f58 homo sapien
Q8ixj5 homo sapien
Q9czb2 mus musculu
O97884 equus cabal
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022458 chlamydomon
Q8ti59 methanosarc
Q8tpy6 methanosarc
Q8tpz8 methanosarc
Q8tpz1 methanosarc
Q7u5x8 synechococc
Q9pps rattus norv
Q8tpy7 methanosarc
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Q8n3r2 homo sapien
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Q8bva0
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Strausberg R.;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032783; AAH32783.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPRO0601; PKD.
Pfam; PF00801; PKD; 1.
SWART; SM0089; PKD; 1.
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Last sequence update)
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Homo sapiens (Human).
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Q97884
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Q8IY46
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                                                                                                             Description
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              Compugen Ltd.
                                     - protein search, using frame_plus_n2p model
   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compus
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Maximum Match 100%
Listing first 45 summaries
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Dendritic cell-associated transmembrane protein (Glycoprotein (Transmembrane) nmb).
GPNMB OR DCHIL.
Buks musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Shikano S., Bonkobara M., Zukas P.K., Ariizumi K.;
"Molecular Cloning of a Dendritic Cell-Associated Transmembrane
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C TISSUE-Salivary gland;
Strausberg R.;
Submitted (APP-2002) to the EMBL/GenBank/DDBJ databases.
R SITA AF322054; AAK14240.1;
EMBL; AF322054; AAK14240.1;
EMBL; BC063375; AAK14240.1;
R MGP; MGT:1934765; Gpmab.
R GO; GO:0005194; F:cell adhesion molecule activity; IDA.
GO; GO:0005194; F:cell adhesion molecule activity; IDA.
GO; GO:0007155; P:neparin binding; IDA.
GO; GO:0007155; P:neparin binding; IDA.
R GO; GO:000831; P:neparin binding; IDA.
R Fam; PF000601; PKD.
R FAM; PR000801; PKD; 1.
R FAMR; SMART; SMO0089; PKD; 1.
R PROSITE; PS00443; GATASE_TYPE_II; 1.
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                                                                                                                                   Prophe ProArg ProHis ClyTrp Lys Trp Ser Phe Val Tyrval Phe His Thr Leu
                                                                                                                                                                           GTGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATAT
                                                                                                                                                                                                                                                                                     AGAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAG
               CCTTTTCCTCACCCCGGATGGAGGATGGAATTTCATCTACGTCTTCCACACTT
                                                                                                                                                            GGTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAAT
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                          Bechner D., Schroder D., Gross G.;
Bachner D., Schroder D., Gross G.;
Bachner D., Schroder D., Gross G.;
Isolation and developmental expression analysis of murine nmb submitted (NOV-1999) to the RMBL/GenBank/DDBJ databases.

EMBL, A1251685, CA865272.1;
AMG: MGI: 1934765, Genmb.

RGO; GO: 00051897; C: integral to plasma membrane; IDA.

RGO; GO: 0008201; F: heparin binding; IDA.

RGO; GO: 0005178; F: integrin binding; IDA.

RGO; GO: 0000178; F: integrin binding; IDA.

RICETPO: IPRO00681; RAD.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
putative transmembrane glycoprotein.
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Matches:
Conservative:
Mismatches:
Indels:
                         CAGGAAAAGGATCCGCTACTCAAAAACCAA 1720
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PROSITE; PSS0093; PKD; 1
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2170.00
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SMART; SM00089; PKD; 1.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
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|ProPheproArgProHisGlyTrpLysLySTrpSerPheValTyrValPheHisThrLeu 180
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                                                                                                                           HisAsnGlnLeuArgGlyTrpSerSerAspGluAsnGluTrpAspGluHisLeuTyrPro
                                                                  GTGTGGAAGCGGGGAACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCG
                                                                               61 ValTrpArgArgGlyAspGlyArgTrpLysAspSerTrpGluGlyGlyArgValGlnAla
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=CS7BL/6J, TISSUE=Skin;

XM MEDINE=22354683; PubMed=12466851;

The FANTOM Consortium,

The FANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

XI "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";

REMEL; AK076347; BAC36306.1; -.

REMEL; AK076347; BAC36306.1; -.

RMED; MG1:1934765; Gpimub.

GG; GG:0005887; C:integral to plasma membrane; IDA.

GG; GG:0005194; F:cell adhesion molecule activity; IDA.

GG; GG:0005176; F:integrin binding; IDA.

GG; GG:0007155; P:cell adhesion; IDA.

GG; GG:0007155; P:cell adhesion; IDA.

RIHERPRO; IPR000683; GATasee_2.

RIHERPRO; IPR000661; PKD.

RITHERPRO; IPR000661; PKD.
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GCAAACAGTGCCCTGATCTCCGTTGGCTTGGCCATALTTGTCACTGTGATCTCCCTC
                                                TIGGTGTACAAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63675 MW; B6AE99DD5DB7C6D0 CRC64;
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Last annotation update)
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Mismatches:
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23,
25,
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01-MAR-2003 (TrEMBLRel, 2)
01-OCT-2003 (TrEMBLRel, 2)
Glycoprotein.
GPNMB.
Mus musculus (Mouse)
                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00801; PKD; 1. SMART; SMO089; PKD; 1. PROSITE; PS00443; GATP PROSITE; PS50093; PKD;
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SEQUENCE FROM N.A.

SEQUENCE FROM STAINS-C57BL/6J; TISSUE-Retina;

MEDLINE-21354683; PubMed=12466851;

The FRATOM Consortium,

At the RIKEN Genome Exploration Research Group Phase I & II Team;

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDMAs.;

IL Nature 420:563-573(2002).;

MEDLI AKO44764; BAC32074.1; -.

REDLI AKO44764; BAC32074.1; -.

REDLI AKO44764; Picell adhesion molecule activity; IDA.

GO; GO:0005124; F:cell adhesion molecule activity; IDA.

GO; GO:0005178; F:integrin binding; IDA.

GO; GO:0005178; F:ntegrin binding; IDA.

GO; GO:0005178; F:ntegrin binding; IDA.

RO; GO:0005178; F:ntegrin binding; IDA.

GO; GO:0005178; F:ntegrin binding; IDA.

THEFPRO; IRRO05681; GARJASE-2.

SER INTERPRO; IRRO05681; GARJASE-2.

SER INTERPRO; IRRO05681; GARJASE-2.
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              CAAGGGAGCATTCCCACGGAGGTCTGTACCATCATTTCTGACCCCCACCTGCGAGATCACC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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PROSITE; PS0093; PKD; 1.
SEQUENCE 574 Aa; 63693 MW; DC0D48485BA2E9D1 CRC64;
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Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 2:
01-OCT-2003 (TrEMBLrel. 2:
Glycoprotein.
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SMART; SM00089; PKD; 1
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SMART; SM00089; PKD; 1.
PROSITE; PS50093; PKD; 1.
                                 572 AA;
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                         GlyProCysProProSerProSerThrProProProProSerThrProProSerPro
                                                   TCAAAACCCACCCTTCTTTAGGACCTGCTGGTGAC
                                                            TTTCAAGCCACCATCACAATTGTAGAGGAATCTTAGAGGTTAACATCATCCAGATGACA
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Xu J., Safadi F.F., Smock S.L., Rosenzweig A.B., Odgren Marks S.C. Jr., Popoff S.N., Owen T.A.;

"Cloning and Characterization of a novel cDNA highly exp osteopetrotic bone.";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF184983; AAF03400.1; -.
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The FANTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

The FANTOM Consortium,

The FANTOM Consortium,

The FANTOM Consortium,

The All Plantysis of the mouse transcriptome based on functional annotation of 60,770 full-length ADNAS.;

L Nature 420:563-573(2002).

R Nature 420:563-573(2002).

R BBL; AK079220; BAC37578-1; ---

R GO; GO:0008152; P:metabolism; IEA.

R InterPro; IPR000601; PKD.

R PFam; PF00801; PKD; 1.

R PRART; SM0089; PKD; 1.

R PROSITE; PS0093; PKD; 1.

R PROSITE; PS0093; PKD; 1.

R PROSITE; PS0093; PKD; 1.
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|121 ArgAsnAspLeuGlyLeuThrSerAspLeuHisVallYrAsnTrpThrAlaGlyAlaAsp
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MEDLINE=22354683; PubMed=12466851;
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Best Local Similarity:
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                                         CTGGAGCTGAGTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAA
                             CACACGTATGTGCTCAATGGAACCTTCAGCTTAACCTCACTGTGAAAGCTGCAGCACCA
                                                                                                                               -----TCAAAACCCACCCTTCTTTAGGACCTGCTGGTGACAACCCC
                                                                                                                                              QBEVAO:
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glycoprotein.
Mus musculus (Mouse)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                              GGACCTTGTCCGCCACCGCCACCACCACCAGACCT---
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STRAIN=CS7BL/6J; TISSUE=Urinary bladder;
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Penlan M., Farmer A.;
"Cloning of human full-length CDSs in BD Creator (TM) System Donor Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC011595; AAH11595.1;
EMBL; AC005082; AAP25337.1;
EMBL; BC016021; C:integral to membrane; IEA.

Hypothetical protein; Transmembrane.

SEQUENCE 206 AA; 23945 MW; 30CBDE6928D73FBD CRC64;
        Homo.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Kalicki J., Kramer J.,
"The sequence of Homo sapiens BAC clone CTA-271G13.",
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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Eutheria; Primates; Catarrhini; Hominidae;
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"Toward a complete human genome sequence.";
Genome Res. 8:1097-1108(1998).
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MEDLINE=99063792; PubMed=9847074;
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Submitted (JUL-2001)
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Submitted (OCT-2000)
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Submitted (MAR-2001)
[6]
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Submitted (JUN-2002)
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Submitted (APR-2003)
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Submitted (MAR-2002)
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SEQUENCE FROM N.A.
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                      NCBI_TaxID=9606;
                                                                            TISSUE=Skin;
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LysGlyAlaThrProMetGluAlaCysThrIleIleSerAspProThrCysGlnIleAla
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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01-DEC-2001 (TrEMBLrel. 19, C.
01-DEC-2001 (TrEMBLrel. 19, L.
01-JUN-2003 (TrEMBLrel. 24, L.
Similar to glycoprotein (Tran
GPNMB).
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AKA MEDLINE=21095660; FUDMEG=1121/851;
A KAWAJ U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
ARAWAJ T., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S.,
A Azawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Satto T., Okazaki Y., Gojobri T., Bono H., Kasukawa T., Saito R.,
A Radito T., Okazaki Y., Gojobri T., Bono H., Kasukawa T., Sakan T.,
A Schriml L. Lowis S., Matsuo Y., Nikaido I., Reole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Nordone P., Ring B., Ringwald M., Mazzarelli J., Mombaerts P.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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HisAsnGlnLeuAsnGlyTrpSerSerAspGluAsnAspTrpAsnGluLysLeuTyrPro
                                                                                                                                                                                                                                         ATATTCCCTAGATGCCAAAAGGAAGGAAGGTGCCAATGGCAACATAGTCTATGAGAAGAACTGC
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                                                                          GTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTG
                                                    GTGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAAGGCCGTGTGCAGGCG
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Mus musculus (Mouse).
Eukaryotai, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection.";
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Last annotation update)
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STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
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SMART; SM00089; PKD; 1.
PROSITE; PS50093; PKD; 1.
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InterPro; IPR006601; PKD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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"Identification and Characterization of T cell defined tumor antigens
"Identification and characterization of T cell defined tumor antigens
in the melanoma model MZ7.";
Thesis (2002), Department of Biological Sciences,
Johannes Gutenberg-University of Mainz, Mainz, Germany.

EMBL; AJ505015; CAD43718.1;
SEQUENCE 206 AA; 24003 MW; 30C8EE5A28D73FBD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                              GACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAA
                                                                                                   HisAsnGlnLeuAsnGlyTrpSerSerAspGluAsnAspTrpAsnGluLysLeuTyrPro
                                                                  GTGTGGAAGCGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAAGGCCGTGTGCAGGCG
                                                                                                                                                            GTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTG
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Conservative:
Mismatches:
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Best Local Similarity:
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Pred. No.:	SCOTES:	3	1 7
Score:	2.18e-53 Length: 644.50 Matches:	λõ	1010
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Query Match DB:		δλ	1012
US-10-039-272	-1 (1-2661) x Q9CZB2 (1-626)	qq	314
δλ	78 TICCIGGGATTICIGCTCCIGGCTGCAAGATTGCCACTIGATGCCGCCAAACGA 131	δλ	1013
DP	aLeuGluGlySerArg	qa	334
ζŎ	132 TITCAIGATOIGCTGGGCAATGAAAGACCTICTGCTTACATGAGGGAGCACAATCAATTA 191	λō	1042
qa		Db	354
Qy	192 AATGGCTGGTCTTCTGATGAAATGACTGGAATGAAAACTCTACCCAGTGTGGAAGGGG 251	ζō	1043
අග	40ThrLysThrTrpAsnArgGlnLeuTyrProGluTrpThr 52	qq	374
Qy	252 GGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGT 311	δ	1058
qu		qo	394
ογ	312 GACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGA 371	λõ	1100
qq	72 AspGlyBroThrLeuValGlyAlaAsnAlaSerPheSerTleAlaLeuHisPheProGly 91	අු	413
δy	372 TGCCAAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGA,TGCAGAAATGAG 428	δ	1124
qu		욥	433
λζ	429 GCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACGCATGGTCAGAGGACAGTGAC 488	Å i	1163
QQ		ag —	453
	489 GGGGAAAAIGGCACCGGCCAAAAGCCAICAIAACGICTICCCTGAIGGGAAACCIIITCCI 548	à	1223
np qu		<u>名</u>	467
oy VQ	549 CACCACCCGGAIGGAGAIGGAATTICAICIACGICIICCACACACATTGGICAGIAI 608	δ	1283
Db		qq	487
ΟY	609 TTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACACGCAATGTGACACTT 668	λõ	1343
qq		qu	507
ολ	669 GGGCCTCAACGAAGTGAACTGTCTACAGAAGACATGGACGGGCATATGTTCCC 725	δλ	1400
qq		qa	527
ζ	726 ATCGCACAAGTGAAAGATGTAGGTAAGGATAACAGATTCCTGTGTTTGTGACTATG 785	ò	1460
Db 1		qq	547
ζ	20	Λō	1520
Dp qu	23	qq	562
oy ,	88	δy	1580
CP qc	236ProbeullePheAlaLeuGlnLeuHisAspProSerGlyTyrLeuAlaGluAla 253	qa	582
λο	94	λō	1625
DP .	27	අධ	602

	::: ::::    aGlnValValLeuGlnAla 293
1010 GCA	1012
294 AlalleProLeuValSerCysGlySerSerProValProGlyTh	ProGlyThrThrAspGlyTyrMet 313
1012	1012
314 ProThrAlaGluAlaProGlyThrThrSerArgGlnGlyThrThrThrLysV	rThrLysValValGly 333
1013GCACCAGGACCTIGTCCGCCACCGCCACCA	1042
334 ThrThrProGlyGlnMetProThrThrGlnProSerGlyThrTh	ThrValValGlnMetPro 353
. 1042	1042
354 ThrThrGluValThrAlaThrThrSerGluGlnMetLeuThrSerAl	rAlaValIleAspThr 373
1043	CACCCAGACCTTCA 1057
374 ThrLeuAlaGluValSerThrThrGluGlyThrGlyThrThrProThrArgProSerGly	 
1058AAACCCACCCCTTCTTTAGGACCTGGTGACAACC	CAACCCCTG 1099
riciuglyProAspAla	-Se
1100GAGCTGAGTAGGATTCCTGATGAA	1123
413 ThrGlnSerSerThrGlySerIleSerProLeuLeuAspAspThrAspThrIl	rAspThrIleMetLeu 432
1124AACTGCCAGATTAACAGATATGGCCACTTTCAAGCCAC	CCACTTTCAAGCCACC 1162
433 ValLysArgGlnValProLeuAspCysValLeuTyrArgTyrGlySerPheSerLeuAl	 
1163 ATCACAATTGTAGAGGAATCTTAGAGGTTAACATCATCAGATGACAGACGTCCTGATG	12
aco memospirevarentes y	aGlulleLeuGin 46
1223 CCGGGGCCGGAAGGTCCCTAATAGACTTGTGGGACCTGCCAAGGGAGGATT 	CCTGCCAAGGGAGCATT 1282             erCysGlnGlyGlyLeu 486
1283 CCCACGGAGGICTGTACCATCATTTCTGACCCCACCTGCGAGATC	CACAGTC 13
	oProAlaGlnArgLeu 506
1343 TGCAGCCCTGTGGATGTGGATGTGTGTCTGACTGACTGGAGACGAACCTT	ACGAACCTTCAAT 1399 ::: sGlnValLeuLysGly 526
1400 GGGTCTGGGACGTACTGTGTGAACCTCACCCTGGGGGATGACACA	reecrereace 14
527 GlySerGlyThrTyrCysLeuAsnValSerLeuAlaAspAlaAsnSerL	
AGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCGCCT	15
047	LeuGlyGln 561
1520 GCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCT	TGATCTCCCTCTTGGTGTAC 1579     :::
ZAAGG	rgggaat 1624
:::   S82 HisArgHisArgLeuLysLysGlnGlySerValSerGlnMetProHi	oHisGlySerThrHis 601
ы	CITICICAACCGIGCA 1666
N	615
1667 AAAGCGTGTTCTTCCCGGGAAACCAAGAAAGGATCCGCTACTCAAAAACCAAGAA 	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1244 TCCCTAATAGACTTTGTGGTGACCTGCCAAGGGAGCATTCCCACGGAGGTCTGTACCATC 1303
CCTTCTTTAGGACCT 1081
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                                                                            GlyHisSerAlaGlnValThrValGlnSerTrpTrpLysProGlnTrpArgGlyThrGln
                                                                                                                                                                                                                                                                                                                                                      1124 AACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                241 ProLeuSerLeuArgValGlnMetProAlaHisSerCysTyrArgArgAsnTyrArgSer
                                                                                                                                                                                                                                                                                                                                                                        281 AspCysValLeuTyrArgTyrGlySerPheSerLeuThrLeuAspIleValGlnGly---
                                                                                                                                    201 MetProLeuGlnArgLeuLysGlylleProProGluValSerAsnSerArgSerLeuLeu
                                                                                                                                                                                                                                                                                                                         261 GlnSerProLeuLeuAspGlyThrAlaThrLeuPheLeuValLysArgGlnValProLeu
                   | | | | ::: |
161 GlnValProThrThrGluValIleSerThrThrProValGlnValProThrAlaGluAsp
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UTON-2003 (TrEMBLrel. 24, Last annotation update)
Melanosomal matrix protein (Fragment).
                                                                                                                    -ATTCCTGATGAA
                                                          1082 GCTGGTGACACCCCCTGGAGCTGAGTAGG----
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SEQUENCE FROM N.A.
MEDLINE=99119493; PubMed=9918878;
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| 141 ValValAsnThrThrProGlyGlnValProThrAlaGluProSerArgThrThrAlaVal 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 ArgAlaLeuValValThrHisThrTyrLeuGluSerGlyProValThrAlaGlnValVal 100
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ArgGlySerGlnThrTyrMetProLeuAlaHisSerArgSerAlaPheThrIleThrAsp
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       ---GluAsnSerProLeuLeuSerGlyGlnGln 625
                                                                                                                                                                                Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                       TISSUESEKIN;

Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;

Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;

"An equine sequence homologous to melanocyte protein 17 (PMEL17)

mapped to chromosome 6623.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF076780; AAC97108.1; -.

InterPro; IPR000601; PKD.

PEam; PF00801; PKD; 1.

SMART; SM00089; PKD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461
101
64
119
153
                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Melanocyte protein 17 (Fragment).
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Mismatches:
Indels:
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Matches:
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                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       49334 MW;
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372.00
37.84%
23.17%
7.67%
                                                                  PRELIMINARY;
                                                                                                                                                                     Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                         461 AA;
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Best Local Similarity:
                                                                                                                                                                                                                NCBI_TaxID=9796;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                147 AlaProAlaProGlyCysGlnLeuValLeuArgGlnAspPheAsnGlnSerGlyLeuTyr 166
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| CysleuAsnValSerLeuAlaAsnGlyAsnGlyLeuAlaValAlaSerThrArgValAla 186
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|ProThralaGlySerThralaGluProLeuLeuValLysArgGlnAlaProGluSer 69
                                                                                                                                                                                                                                                                                                                                                                      70 GluProThrGlyCysValLeuTyrArgTyrGlySerPheSerThrGluLeuAsnIleVal
 R., Bister K.;
by doxycycline-controlled expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 GlySerGlyAsnSerValGluLeuThrValThrCysGluGlySerLeuProGluGluVal
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|CysThrValValAlaAspAlaGluCysArgThrAlaGlnMetGlnThrCysSerAlaVal
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71
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Mismatches:
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                                                        EMBL, AF077328; AAD12180.1; -. GO: 0005198; F:structural molecule activity;
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Oberst C., Hartl M., Weiskirchen Conditional cell transformation of the MC29 v-myc allele."; Virology 253:193-207(1999).
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26785 MW;
                                                                                                                                                          3.84e-17
271.50
48.03%
31.00%
5.60%
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                                                                                                                270 AA;
                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                   Matrix protein.
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Pred. No.:
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LeuGlyGlnAlaProLeuLeuValGlyIleLeuLeu 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyProAspAlaSerProLeuLeuProThrGlnSerSer----ThrGlySerIleSer
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                                                                                                                                                        MEDINE=20063689; PubMed=10594241;
Martinez-Esparza M., Jimenez-Cervantes C., Bennet D.C., Lozano J.A.,
Solano F., Garcia-Borron J.C.;
"The mouse silver locus encodes a single transcript truncated by the
                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                            236 AA; 24293 MW; 3ECB812D4DF10EE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             236
62
31
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Mutant matrix melanosomal protein silver (Fragment)
SI.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                         Mamm. Genome 10:1168-1171(1999)
EMBL; AF119092; AAF19761.1; -.
MGD; MGI:98301; Si.
                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like
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247.50
47.69%
31.79%
5.10%
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                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                             silver mutation."
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                               1077 GACCTGCTGGTGACAACCCCCTGGAGCTGAGTAGGATT---CCTGATGAAAACTGCCAGA 1133
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                                                                                                                                                 896
                                                                                                                                                                   -GlnProValA 121
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                                                        121 laargGlyPheValValLeuProIleThrGluPheLeuValGlyAspLeuValValThrG
                                                                                                            897 ACTACAAGTGGAGCTICGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTA
                                                                                                                                                                                                                                                                                       ------GluTrpGluGluValGluProAspAlaThrArgAlaV
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                               - AACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAG
                                                                                       ---TCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCC
                                                                                                                                                   CCATTATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTA
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 112 laAspCys-
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                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TCCTGG
                                                                                                                                                                                                                                                                                                     Ansorge W., Wirkner U., Mewes H.W., Weil B., Wiemann S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC030793; AAH30793.1; -. EMBL; AL084348; CAD39013.1; -.
                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                              CRC64
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1112
67
162
142
                                                              01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Similar to QNR-71 protein (Hypothetical protein).
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Matches:
Conservative:
Mismatches:
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                                                  Created)
                     PRT;
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                                                (TrEMBLrel. 22, (TrEMBLrel. 22, (TrEMBLrel. 24,
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198.50
37.06%
23.19%
4.09%
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PROSITE; PS50093; PKD; 1.
Hypothetical protein.
SEQUENCE 423 AA; 46988
                     PRELIMINARY;
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Submitted (MAY-2002)
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GlySerLeu-
                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                                       NCBI_TaxID=9606;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                    -----AAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCGTGGGC 332
                                                                                                                                                                                                                                                                                                                                                                                                 TCAAATATAAACATTTGCGGTGAACCTGATATTCCCTAGAIGCCAAAAGGAAGATGCCAAT 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAA 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTG 746
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141 lnAsnThrSerLeuProTrpProSerSerTyrLeuThrLysThrVal------LeuL 158
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                                                                                                                                                                                                                                                                                                                          ValTrpSerArgLeuGlyArgIleLeuTrpLeuAlaCysLeuLeuProTrpAlaProAla 24
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                                Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                           ----ICCIGG-
                                                                                      TISSUE-Amygdala;
Ansorge W., Wirkner U., Newes H.W., Weil B., Wiemann S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL893449; CAD39014.1; -.
InterPro; IPR000601; PKD.
PROSITE; PS50093; PKD; 1.
                                                                                                                                                                    737509A3F8263A4F CRC64;
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Matches:
Conservative:
Mismatches:
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                     Homo sapiens (Human).
Bukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                         Hypothetical protein.
SEQUENCE 435 AA; 48329 MW;
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23.19%
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Best Local Similarity:
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                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GICIGCIGACTGIGAGACGAACCITCAATGGGICTGGGACGTACTGIGIGAACCICACCC 1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1134 TT---AACAGATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGG 1190
                                                                                                                   euTyrSerTrpAspPheGlyAspGlyThrGlnMet---ValThrGluAspSerValValT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ProGluCysLeuProLeuGluGluGluGlyGluCysHisProValSerValAlaSerThrA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 laGluAsnIleIleSerLysThrHisGlnTyrHisLysTleGlnValTrpProSerArg- 336
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                                                                  1191 TTAACATCATCCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euAsnPheLeu-------GlySerProbroLeuThrValCysTrpArgLeuIys-
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earch completed: September 10, 2004, 15:48:29 ob time : 243 secs

Appl Appl Appl Appl Appli

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Run on:

Sequence:

Minimum DB Maximum DB

Searched:

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Sequence 44, Appl
Sequence 31611, A
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 7998, Appl
Sequence 7998, Appl
Sequence 7998, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 90, Application US/09985799;
Patent No. RE38392;
GENERAL INFORMATION:
APPLICANT: THOMSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22,
                             Sequence
                                                                                                                                    Sequence
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US-08-417-174-121
US-08-267-439-121
US-08-388-8528-2
US-09-073-138-121
US-08-417-174-27
US-08-417-174-27
US-09-007-961-27
US-09-267-439-27
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US-09-388-8528-38
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US-08-388-8528-38
US-08-388-8528-36
US-09-996-998
US-08-991A-31611
US-09-976-54-64
US-09-976-54-01
US-09-976-54-01
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US-08-325-267A-2
US-09-281-766-19
US-08-658-136-5
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: 06-No. RE3392-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEPRAX: 202-639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BAKER & BOTTS, L.L.P.
STRET: 1299 Pennsylvania Avenue,
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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  RESULT 1
US-09-985-799-90
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  Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-VOG92004 144224 21675/app query.fasta_1.2823
-V=/cgn2_1/USFPO.spool_P/USI0039272/runat_07092004 144224 21675/app query.fasta_1.2823
-DS=ISSNed Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCIA-0.1
-LOOPEXT=0 -UNITS=Eits -START=1 -ENN=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pot -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US10039272 @CGN 1 1 48 @runat 07092044 144224 21675 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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225, App
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                                                                                                                                                                                                                                                                      Description
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                              - protein search, using frame_plus_n2p model
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US-08-594-031-90
US-09-643-225
US-09-542-615A-225
US-09-542-615A-225
US-09-6421B-225
US-09-383-586-36
US-09-985-799-100
US-09-985-799-102
US-09-985-799-102
US-08-594-031-102
US-08-594-031-102
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                                                                                                                                      September 10, 2004, 15:32:29
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Database

Result No.

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Patent No. 5783182

GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175

CORRESPONDENCE ADDRESS:
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US-08-594-031-90
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Matches:
Conservative:
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S
                                                STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-SENSE: NO
CRIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO
                                 LENGTH: 560 amino acids
TYPE: amino acid
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2999.00
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              INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
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                 N.
         STREET: 1299 Pennsylvania Avenue, N. STREET: 1299 Pennsylvania Avenue, N. STREET: 1299 Pennsylvania Avenue, N. STREET: 20004-2400
COMPUTE: BEADLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEMO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION NUMBER: 6/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 36,902
REGISTRATION NUMBER: 36,902
REGISTRATION NUMBER: 36,902
REGISTRATION NUMBER: 36,902
                                                                                                                                                                                                                                                                    0A146-0110
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 90: SEQUENCE CHARACTERISTICS: LENGTH: 560 amino acids TYPE: amino acid
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2999.00
99.82%
99.82%
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Best Local Similarity:
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TOPOLOGY: lir
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<b>+</b> + €	20 AGAAATGAGGCTGGTTATCTGCTGATCCATATGTTACAACTGGACAGGATGGTCAGGG 47	480 GACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATATTpThrAlaTrpSerGlu 14 480 GACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAA 53	11 Propheronial Strand Control of the Control of th	600 GGTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAAT 6	660 GTGACACTTGGGCCTCAACTCATGGAACTGACTGTCTACAGAAGACATGGACGGGCATA  [	720	780 ACTAIGITCCAGAAGAACGAICGAAATICAICCGACGAAACCIICCC-AAAGAICTCCCC 8	839 ATTATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCATTAAC 89 [	899 TACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTT	/ 959 CACACGTATGTGCTCCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCGGCACCA 1018	1019 GGACCTTGTCCGCCACCGCCACCACCAGACCTTCAAAACCCACCC	/ 1079 CCTGCTGGTGACAACCCCTGGAGCTGAGATTCCTGATGAAAACTGCCAGATTAAC 1138	1139	1199 ATCCAGATGACACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTT 1258	1259	1319	1379 ACTGIGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGAACCTCACCCTGGGGGAT 14 [
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Skeiky, Yasir A.W.
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AMD DIAGNOSIS OF LUNG CANCER TILE REFERENCE: 210121.45509
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
SOFTWARE: FastsEQ for Windows Version 3.0
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      ThrValArgArgThrPheAsnGlySerGlyThrTyrCysValAsnLeuThrLeuGlyAsp
                              GACACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAAGAGCCCAGCCTCG
                                              CCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACT
                                                                                                                              GTGATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCT
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Sequence 36, Application US/09383586

Batent No. 6242419

GENERAL INFORMATION:

APPLICANT: Strachan, Lorna

APPLICANT: Abernethy, Nevin

APPLICANT: Onruer, Rene

APPLICANT: Curble, Anand

APPLICANT: Curble, Anand

APPLICANT: Compounds isolated from stromal cel:

TITLE OF INVENTION: Compounds for their use

TITLE OF INVENTION: and methods for their use

FILE REFERENCE: 11000.1037c1

CURRENT APPLICATION NUMBER: US/09/383,586

URRENT FILING DATE: 1999-08-26

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 36

SEQ ID NO 36
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Mismatches:
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CRGANISM: Mouse
US-09-383-586-36
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US-09-383-586-36
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197, 970B
FILING DATE: 23-No. 6664385-1998
CLASSIFICATION: <unimal color of the c
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FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NEMBER: Levine, Leslie M.
REGISTRATION NUMBER: 35,245
REFERENCE/DOCKET NUMBER: A010 PCT
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Catherine A. Hession
Takaharu Idhimura
Henry Wei
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STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
-09-197-970B-5
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OF INVENTION: MODULATORS
R OF SEQUENCES: 7
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TELEPHONE: (617) 679-2810
TELEFAX: (617) 679-2838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09197970B Patent No. 6664385 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS
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                          Conservative:
Mismatches:
Indels:
                                                                                              US-10-039-272-1 (1-2661) x US-09-197-970B-5 (1-572)
                Matches:
 Length:
4.94e-213
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82.57%
69.54%
44.37%
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519 AACGICTICCCTGAIGGGAAACCTITICCTCACCACCCGGAIGGAGAAGAIGGAATTIC 578
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Mismatches:
Indels:
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PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PAPLICATION DATA:

FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:

TELEX: <university of the control of the c
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Matches:
                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-No. RE38392-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-985-799-100
SOFTWARE: FastSEQ Version 1.5
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  301 HisThrTyrValLeuAsnGlyThrPheAsnPheAsnLeuThrValGlnThrAlaValPro 320
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APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCES: L.I.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
                                                         GGACCITGICCGCCACCACCACCACCACCAGACCI
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ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
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Qy         1659 ACCGTGCAAAAGCCGTCTTCTCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACC 1718           Db         361 ShArgAlaLysAlaValGlyAshLysAsh 372           Qy         1719 AAGAATTTAAAGGAGTTTCT 1738           Db         373LysGlyValSer 376	RESULT 10 US-09-985-799-102 ; Sequence 102, Application US/09985799 ; Patent No. RE38392 ; GENERAL INFORMATION: ; APPLICANT: THOMPSON, Timothy C. ; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES ; NUMBER OF SEQUENCES: 175 ; CORRESPONDENCE ADDRESS:	ADDRESSEE: BAKER & BOTTS, L.L.P. STREET: 1299 Pennsylvania Avenue, N.W. CITY: Washington STATE: DC COUNTRY: USA ZIP: 20004-2400 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPREMATING SYSTEM: Dos	CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/09/985,799 FILING DATE: 06-No. RE38392-2001 CLASSIFICATION - UNKNOWN> PRIOR APPLICATION DATA:  APPLICATION NUMBER: US/08/594,031 FILING DATE: 30-APPLICATION NUMBER: 00/006,838 FILING DATE: 16-NOV-1995 ATTORNEY/AGENT INFORMATION: NAME: Remenick, James HATCHEN MAME: Remenick, James	TELECOMMUNICATION NUMBER: 08.902   TELECOMMUNICATION NUMBER: 08.902   TELEPHONE: 20.6.639-7700   TELEPHONE: 20.6.639-7700   TELEPA: 20.6.639-780   TELEFA: 20.6.639-780   TELEFA: 20.6.639-770   TENGTH: 376 amino acida   TYPE: amino acida   TYPE: amino acida   TYPE: amino acida   TOPEOLOGY: linear   TOPEOLO	
S79 ATCTACGTCTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGA 638	AGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACA	B19 ACCITCCCAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGGCCACTTCC 678  183 hrLysAspMetAsp		SerS SerS IGTA 1   1   1   1   1   1   1   1   1   1	1916   19

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224

1298

--TrpSerS

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1418

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1538

----SerValA 361

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1119 ATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGG 1178
                                                                                              1059 AACCCACCCTTCTTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGAGTAGGATTCCTG 1118
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Patent No. 5783182
GENERAL INFORMATION:
APPLICANT: THOMSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
CORRESPONDENCES: 175
CORRESPONDENCE BAKER & BOTTS, L.L.F.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Mashington
STATE: DC
COUNTRY: USA
                                                                 erThrAsnHisThrValAsnHisThrTyrVal---AsnGlyThrSerAsn-
     --GlyAspAsnThrGly-
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                                                                                                            224 hrValLysAlaAlaAla-----GlyCys---
  --AsnTyrLysTrpSer
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ValHisThrGlyTyrLys------GlyArgCysSerValArg 137
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80 ValTyr-----LysAsnCysArgAsn---AlaGly---SerAlaAsp---TyrValTyr 94
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Matches:
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                                                     ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
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950.50
59.31%
54.56%
     single
                                peptide
NO
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: pept;
HYPOTHETICAL: NO
                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-594-031-100
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Pred. No.:
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----HisHisGlyTrpArgArgTrpAsnTyr
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126 ValHisThrGlyTyrLys----
                 112 Asnval-----AspGlyLys
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299
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177
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Matches:
Conservative:
Mismatches:
Indels:
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                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT PAPPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-DAN-1996
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REGISTRATION NUMBER: 36,902
REGISTRATION NUMBER: 36,902
REFERENCEY/DOSCYTEM
TELECOMMUNICATION INFORMATION:
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-594-031-102
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Pred. No.:
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Query Match:
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25 LysValèroArgAsnGlnAspTrpLeuGlyValSerArg37  180 CACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAACTCTACCCA 239	GTGTGGAAGCGGGGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCGTGTGCAGGCG					519 AACGICTICCTGAIGGGAAACCTITICCTCACCACCCGGAIGGAAGAIGGAAITIC 578 :::::::::::::::::::::::::::::::::::	63		699 AGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAGATGTGTACGTGGGGA 755		816 GAAACCTTCCC-AAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATCTAGCCAC 874 :::	875 TICCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTT 934 :::	935 GTTTCCACCAATCATACTGTGAATCACGTAIGTGCTCAATGGAACCTTCAGCCTTAAC 994 :::	10		310 ThrAspGlyHisArgProThrAlaGluAlaProAsnThrThrAlaGlyGlnValProThr 329	1039 1039 330 ThrGluvalValGlyThrThrProGlyGlnAlaProThrAlaGluProSerGlymhymhy 240		350 SerValGlnValProThrThrGluValIleSerThrAlaProValGlnMetProThrAla 369
90 AQ	, çy	o da	S SS	6 G	<i>ò</i> ₽	Qy Dp	Qy Dp	\(\delta\)	Sy Dp	λ d d	QY QD	ko qa	y Sy Sy	<i>₹</i> 0	٨	qa	da da	ờ	qa
Db 347TyrAsnAsnSerGlyAsnValValArgSerLysGlySerValA 361  Qy 1659 ACCGTGCAAAAGCCGTGTTCTTCCCGGGAAACGGAAAAGGATCCGCTACTCAAAAACC 1718  Db 361 snArgAlaLysAlaValGlyAsnLysAspLysAsn 372	Oy 1719 AAGAATTTAAAGGAGTTTCT 1738  Db 373LysGlyValSer 376	RESULT 13 US-08-417-174-121 ; Sequence 121, Application US/08417174 ; Patent No. 5844075	; GENEKAL INFORMATION: ; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, ; APPLICANT: STEVEN M. MELANOMA ANTIGENS AND	; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC; TITLE OF INVENTION: METHODS; NUMBER OF SEQUENCES: 126; CORRESPONDENCE ADDRESS:	; ADDRESSEE: MORGAN & FINNEGAN, L.L.P. ; STREET: 345 PARK AVENUE ; CITY: NEW YORK ; STATE: NEW YORK	AD AD	COMPUTER: IBM PC COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII CURRENT APPLICATION DATA:	돈 있는	- E	REFERENCY   DOWNER: 37,341   REFERENCY   DOWNER: 2026-4124US1   TELECOMMUNICATION INFORMATION:   TELECOMMUNICATION INFORMATION: 1 TELECOMMUNICATION: 1.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	21 0 Kg v	### ## 21 P	8-417-174-121 nment Scores:		12.23% Indels: 2 Gaps:	-10-039-272-	OY 66 TGTCTCTACTATTTCTGGGATTTCTGCTCCTGGCTGCAAGATTGCTGATGCCCCC 125  Db	GGAG	

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Percent Similarity:
Best Local Similarity:
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                                                         390 AlaGluMetSerThrProGluAlaThrGlyMetThrProAlaGluValSerIleValVal 409
                                                                                                               410 LeuSerGlyThrThrAlaAlaGlnValThrThrThrGluTrpValGluThrThrAlaArg 429
                                                                                                                                                                         430 GluLeuProlleProGluProGluGlyProAspAlaSerSerlleMetSerThrGluSer 449
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370 GluSerThrGlyMetThrProGluLysValProValSerGluValMetGlyThrThrLeu 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 121, Application US/09267439
| Patent No. 627078
| GENERAL INFORMATION:
| APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
| APPLICANT: STEVEN A.
| TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC;
| TITLE OF INVENTION: METANOSA ANTIGENS AND
| TITLE OF INVENTION: METANOSA ANTIGENS AND
| TITLE OF SEQUENCES: 126
| CORRESPONDENCE ADDRESS:
| ADDRESSER: MORGAM & FINNEGAM, L.L.P.
| STREET: 345 PARK AVENUE
                                                                                                                                                  ----CCACCACCAGACCTTCAAAACCC----
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEW YORK
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CITY: NE
STATE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IleIleAshGlySerGlnValTrpGly 117
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Mismatches:
Indels:
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- GlyGlnProValTyrProGlnGluThrAspAspAla-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 37,341
TELEPHONE: (212) 754-6849
TELEPHONE: (212) 751-6849
TELERA: 421792
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-039-272-1 (1-2661) x US-09-267-439-121
                                                                             US/09/267,439
                PC-DOS/MS-DOS
IBM PC COMPATIBLE
                OPERATING SYSTEM: PC-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.45%
25.34%
12.23%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: Un'
TOPOLOGY: Unknown
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Oy 1232 TGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCACGGAG 1291	GACACAGCCTGGCTCTCACGAGCACCCTG           :::           ThrAsnSerLeualaValValSerThrGln CCTTTAAGGATGGCAAACAGTGCCCTGATC	584 LeuilemetProGlyGlnGlualaGlyLeuGlyGlnValProLeuile 599 1529 TCCGTTGGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAA 1585	RESTLT 15 US-08-388-852B-2 ; Sequence 2, Application US/08388852B ; Patent No. 6500919 ; GENERAL INFORMATION: ; APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav. ; TITLE OF INVENTION:	chicopes 38 38S: Gosse Jan 7an Leydenl	COUNTRY: the Netherlands  ZIP: 6525 EX  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)	LICATION DATA:  N NUMBER: US/08/388,852B  NR SEQ ID NO: 2:  PRACTERISTICS:  ARACTERISTICS:  In acid  linear  linear  NO NO NO NO NO	: : :: :: :: :: :: :: :: :: :: :: :: ::
Oy 579 ATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGA 638  150 VallyrvalrpLysThrTrpGlyGlnTyrTrpGlnValLeuGlyGlyProValSerGly 169  639 GTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAGTGACTGTTAC 698  170 LeuSerlleGlyThrGlyArgAlaMetLeuGlyThrHisThrMetGluValThrValTyr 189  639 AGAAGACATGGACGGGCATATGTCCCATCGCACAAGTGAAGATGTACGTGGTA 755  190 HisArgArgArgGlySerArgSerTvvalProfessishish Characacara 1500 HisArgArgGryCyristish Characacara 1500 HisArgArgGryCyragargalyarish Characacara 1500 HisArgArgGryCyragargargargargargargargargargargargarga	756 ACAGATCCAGATTCTGTGACTATGTTCCAGAAGAACGATCGAAATTCATCCGAC 815	rGly GTTT	935 GTTTCCACCAATCATACACATATCACGTATGTGCTCAATGGAACCTTCAGCCTTAAC 994 :::   :::   1	1039 1039 310 ThraspGlyHisargProThralaGluAlaProAsnThrThralaGlyGlnValProThr 329 1039	330 ThrGluValValGlyThrThrProGlyGlnAlaProThrAlaGluProSerGlyThrThr 349 1039 1039 350 SerValGlnValProThrThrGluValIleSerThrAlaProValGlnMetProThrAla 369	Gluse	

126 AAACGATTICAIGHIGIGCIGGGCAAIGAAAGACCITCIGCITACAIGAGGGAG 179	qa	350 Ser
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GlnLeuArgIntlySalatrpAshatgetined17trto	λō	1039
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579 ATCTACGTCTTCCACACTTGGTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGA 638	λ δ	504 Ser
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639 GTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTAC 698 :::   :::	2 A	
75	λ	
90 HisArgArgGlySerArgSerTyrValProLeuAlaHisSerSerSerAlaPheThr11e 20	q ;	544 Val
756 ACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATTCATCCGAC 815	Š 15	
:::    210 ThrAspGlnValProPheSerValSerValSerGlnLeuArgAlaLeuAspGlyGlyGs	e	
816 GAAACCTTCCC-AAAGATCTCCCCCATTATGTTTGATGTCCTGATTCATGATGTCGTAGCCAC 874	Š	114 6041
:::     ::::::      ::::::     ::: :::	3 8	1529 700
875 TTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTT 934 :::	q <sub>Q</sub>	
	Search Job ti	ch completed: time : 78.5 s
310 ThrAspGlyHisArgProThrAlaGluAlaProAsnThrThrAlaGlyGlnValProThr 329		
1039		

GTACTGTGTGAACCTCACCCTGGGGATGACACAAGCCTGGCTCTCACGAGCACCTG 1468 TICIGIICCIGACAGAGACCCAGCCICGACTITAAGGAIGGCAAACAGIGCCCIGAIC 1528 1039 1039 CIGIACCATCATITICIGACCCCACTIGCGAGATCACCCAGAACACAGGTCTGCAGCCCT 1351 GGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTC---AATGGGTCTGGG 1408 ACCCTTCTTTAGGACCTGCTGACAACCCCCTGGAGCTGAGTAGGATTCCTGAT 1120 1291 A------AACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCACATT 1171 AGAGGGAATCTTAGAGGTTAACATCAȚÇCAGATGACAGACGTCCȚGATGCCGGȚGCCA 1231 489 409 userGlyThrThrAlaAlaGlnValThrThrThrGluTrpValGluThrThrAlaArg 429 ethrGlySerLeuGlyProLeuLeuAspGlyThrAlaThrLeuArgLeuValLysArg 469 503 523 aserThrGlyMetThrProGluLysValProValSerGluValMetGlyThrThrLeu 389 uLeubrollebroGluProGluGlyProAspAlaSerSerIleMetSerThrGluSer 449 CGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTTTGGTGTACAAAAA 1585 GCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCACGGAG .ValGlnValProThrThrGluValIleSerThrAlaProValGlnMetProThrAla aGluMetSerThrProGluAlaThrGlyMetThrProAlaGluValSerIleValVal ----CCACCACCAGACCTTCAAAACCC

earch completed: September 10, 2004, 15:52:45 ob time : 78.5 secs

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DESCRIPTION: SEQ ID NO: 91:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
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/cgn2_6/ptodata/2/ina/6A_COMB.seg:*
/cgn2_6/ptodata/2/ina/eDCCOMB.seg:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seg:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seg:*
          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-197-9708-4

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US-09-643-597-121

US-09-480-884A-105

US-09-480-884A-121

US-09-542-615A-121

US-09-542-615A-121

US-09-542-615A-121

US-09-60-421B-105

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                                                                                                                                                                                                                                                                                                                                                         682709 seqs, 277475446 residues
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                                                                                     - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum Match 1008
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APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
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US-09-606-421B-5
US-09-221-107-5
US-09-285-79-113
US-08-594-031-113
US-09-985-799-105
US-09-985-799-115
US-08-594-031-115
US-09-985-799-92
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US-08-594-031-94
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US-08-594-031-23
US-08-594-031-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SPETATING SYSTEM: DOS
SOFTHARE: PASLSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 16-NO. RE38392-2001
CLASSIFICATION LUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 0A146-0110
                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
                                                                                                                                                                                                                                                                                                                                                                     Sequence 91, Application US/09985799
Patent No. RE38392
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: CURKNOWNS
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20004-2400
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SAAGCTACTATTGATTA 2066 AGCTTTCCATGTAACTG 2126 AAGCTAACTGAATCCCA 2186 TTGTTTCTGAAGCTCA 1766 |||||||||||||||| |TGTTTCTGAAGCTCA 1799 CATGTTGTGAAACTGAT 1946 TTGGTGTACAAAAAC 1586 ||||||||||||||||| TTGGTGTACAAAAAC 1619 AGAAGCAAAGGCCTGA 1646 ||||||||||||||| |AGAAGCAAAGGCCTGA 1679 TATAGGTTAAATGTCA 1886 GCAAACAGTGCCCTGA 1526 TTTCAAGCCACCATCA 1166 GACGTCCTGATGCCGG 1226 CAAGGGAGCATTCCCA 1286 ACCTTCAATGGGTCTG 1406 

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                                                                                                                                                                                                Length 2669,
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                                                                                                                                                                                            Score 2547.8;
Pred. No. 0;
                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                       SOURCE:
DESCRIPTION: SEQ ID NO: 101:
         INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 2669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                               ANTI-SENSE: NO FRAGMENT TYPE: <Unknown>
                                                                                                                                                                                          95.78;
                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                  Matches 2591; Conservative
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                       ORIGINAL
SEQUENCE
                                                                                                                                                                US-09-985-799-101
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GTGACAACCTACTTTGCTTGGCTGAGTGAATGATATTCATATTCATATTCATTATTCCA
                                      CTTCAATACACACTCATGAACTCCTGATGGAACAATAACAGGCCCAAGGCCTGTGGGTATGA
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: 06-NO. RE38392-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                 2607 -AAAATGAGGGAAGAGACAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 101, Application US/09985799
Patent No. RE38392
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: BAKER & BOTTS,
STREET: 1299 Pennsylvania CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
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US-09-985-799-101
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Pred. No. 0;
0; Mismatches
                                                                             0A146-0110
                 60/006,838
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,83
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A14
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 202-639-7700
                                                                                                                                    INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 2669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                  Query Match 95.7%;
Best Local Similarity 99.2%;
Matches 2591; Conservative
                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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US-08-594-031-91
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         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-196
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION TOWN-1995
ATTORNEY/AGENT INFORMATION:
NAMME: Rementick, James
REGISTRATION NUMBER: 36,902
RELECOMPUNICATION INFORMATION:
TELLEPAN: 202-639-7700
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INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 2669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 99.2
Matches 2591; Conservative
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20004-2400
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CRIGINAL SOURCE:
US-08-594-031-101
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Patent No. 5783182
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
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56 60 62	TGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCA TCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAG 	SAAATT	TGATC 86	PACTACAAGTGGAGCTTCGGGGATAATACTG 92	TTCA 98	987 GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCACCACCACCACCACCACCACCACCACCACCAC	ACAACCCCTGGAGCTGA 1	DACTITCAAGCCACCAICA	1167 CAATTGTAGAGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGG 1226 	CTGCCAAGGGAGCATTCCCA 12	1287 CGGAGGTCTGTACCATCATTTCTGACCCACCTGCGAGATCACCCAGAACACAGTCTGCA 1346 	1347 GCCCTGTGGATGTGGATGTGTGTGTGGTGAGACGAACCTTCAATGGGTCTG 1406 		CTGA	AAAAC 158       AAAAC 161	1587 ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCTGA 1646 

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                                                                                                            Henry Wei
Richard L. Cate
RICHARD MODULATORS OF TISSUB REGENERATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,970B
FILING DATE: 23-NO. 6664385-1998
CLASSIFICATION: <university contains the contains th
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Pred. No. 1.3e-216;
0; Mismatches 443;
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REGISTRATION NUMBER: 35,245
REGISTRATION INFORMER: A010 PCT TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 679-2810
TELEFAX: (617) 679-2838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,228
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
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LOCATION: 107..1822
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
    GENERAL INFORMATION:
APPLICANT: Michele Sanicola-Nadel
Joseph V. Bonventre
Catherine A. Hession
                                                                                                                                                                                                                                            ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
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STRANDEDNESS: single
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74.1%;
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                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02142
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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1458 1428 1518	OY 1488 ACCCAGCCTCGCCTTTAAGGATGGCAACAGTGCCCTGATCTCGTTGGCTGCTTGGCCA 1547  Db 1578 ACCTAGGCTCCCCTCTGAGAACAGTGAATGTGTGTCCTGATCTCCATTGGCTGCTGGCCA 1637	OY 1548 TATITGICACIGIGALCICCICITGGIGIACAAAAAACACAAGGAATACAACCAAIAG 1607	QY 1608 AAAATAGTCCTGGGAATGTGGTCAGAAGGCGTAGGGGTGTCTTTCTCAACGGTGCAA 1667	1668	OY 1728 AAGGAGTITCTIAAAITICGACCTIGTITCIGAAGGICCATITCAGIGCCATIGAUGIG 1787  Db 1818 IGCTCTAAGICTICACTCICACTCTGACTGGGAACCCACTCTICTGIG-CAIGIAIGIG 1876	QY 1788 AGAIGTGCIGGAGIGGCIATITAACCTITITITCCIAAAGAITAIIGITAAAIAGAI 1843 	Oy 1844 ATTGTGGTTTGGGGAAGTTGAATTTTTATAGGTTA 1879  Db 1937 ATCATGGTTTAGGGAGGGTAGTTAATTGGCATTTA 1972	H (3)	<pre>// Patent No. 6242419 // PENERAL INFORMATION: // APPLICANT: Strachan, Lorna // APPLICANT: Sleeman, Matthew</pre>	APFLICANT: Oblight, Nevin APPLICANT: Orrust, Rene APPLICANT: Anand APPLICANT: Muxison, Greg		CURKENT FILING DATE: 1999-08-26 NUMBER OF SEQ ID NOS: 38 SOFTWARE: FastSEQ for Windows Versi SEQ ID NO 27	; LENGIH: 2213 ; TYPE: DN ; ORGANISM: Mouse US-09-383-586-27	Query Match Best Local Similarity 74.1%; Pred. No. 6.7e-216; Matches 1404; Conservative 0; Mismatches 437; Indels 54: Gans 4.	99 99 99 99 99 99 99 99 99 99 99 99 99		

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Sequence 105, Application US/09643597; Patent No. 6426072; GENERAL INFORMATION: APPLICANT: Wang, Tongtong; APPLICANT: Fan, Liqun APPLICANT: Kalos, Michael D.
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OTHER INFORMATION: Where n is
           NAME/KEY: modified_base
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                     ACCCCACCTGCGAGATCACCCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGTGAGATGT
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APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.45501
CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US/09/103,912A
CURRENT FILING DATE: 1998-07-18
PRIOR APPLICATION NUMBER: 09/40,802
PRIOR PILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 105
LENGTH: 619
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GENERAL INFORMATION:
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OTHER INFORMATION: Where n is a,
NAME/KEY: modified_base
LOCATION: (527)
OTHER INFORMATION: Where n is a,
NAME/KEY: modified_base
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20.5%; Score 545.6; DB 4;
Best Local Similarity 93.2%; Pred. No. 3.2e-108;
Matches 577; Conservative 0; Mismatches 41;
                              CCATION: (564)

OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified base
CCATION: (566)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified base
CCATION: (575)
OTHER INFORMATION: Where n is a, c, g or t
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                                  APPLICANT: incore, .....,
APPLICANT: incore, dary R.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: McMeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT FILING DATE: 200-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 105
LEBNOTH: 619

WINDER OF SEQ ID NOS: 100 NOS: 10
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20.5%; Score 545.6; DB 4;
Best Local Similarity 93.2%; Pred. No. 3.2e-108;
Matches 577; Conservative 0; Mismatches 41;
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CCATION: (1)...(619)
CTHER INFORMATION: n = A,T,C or
US-09-643-597-10
Chaitanya S.
                     Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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ORGANISM: Homo sapien
FEATURE:
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                                                                                          APPLICANT: Address Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Horser, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Washy, Aijun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Momerall, Parricia D.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERRICE 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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FastSEQ for Windows Version 3.0
US-09-643-597-121
; Sequence 121, Application US/09643597
; Patent No. 6426072
; RENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
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NAME/KEY: misc feature
LOCATION: (1)...(619)
OTHER INFORMATION: n = A,T,C or
US-09-643-597-121
                                                                       Wang, Tongtong
Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapien
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Best Local Similarity
Matches 577; Conserv
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GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
FAPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERRENCE: 210121.4556
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 3.2e-108;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                       Sequence 121, Application US/09480884A Patent No. 6482597
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; OTHER INFORMATION: n = A,T,C or
US-09-480-884A-121
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Best Local Similarity 93.2%;
Matches 577; Conservative
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Sequence 105, Application US/09480884A

Sequence 105, Application US/09480884A

GENERAL INFORMATION:

SAPLICANT: Wang, Tongtong

APPLICANT: Hosken, Nancy A.

APPLICANT: Ranger, Michael D.

APPLICANT: Kanger, Michael D.

APPLICANT: Kanger, Michael D.

APPLICANT: Kanger, Michael D.

APPLICANT: Kanger, Michael D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REPERENCE: 21011.455C6

CURRENT FILING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 330

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 105
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Pred. No. 3.2e-108;
0; Mismatches 41;
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; OTHER INFORMATION: n = A,T,C or G
US-09-480-884A-105
                                                                                                             2610 ATGAGGGAAGAGACAAAAA 2628
                                                                                                                                                 601 AAGTGGTGGGAAAAAA 619
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Best Local Similarity 93.2%;
Matches 577; Conservative
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US-09-480-884A-105
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	REBULT 12 Sequence 105, Application US/03542615A APPLICANT: MOMENTALY STORT AND WETHOUS FOR THERAPY ITILE OF INVENTION: Chaltary's S. APPLICANT: Horker, Cary R. APPLICANT: Horker, Cary R. APPLICANT: Horker, Cary R. APPLICANT: Animosty S. 200-0-14 APPLICANT: Horker, Cary R. APPLICANT: AND WETHOUS R. APPLICANT: Horker, Cary

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 121
LENGTH: 619
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Penger, Garry R.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
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Matches 577; Conservative
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US-09-606-421B-121
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Patent No. 6531315

GENERAL INFORMATION:

APPLICANT: Wang, Tidun

APPLICANT: Ralos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Asmuel X.

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER

FILE REFERENCE: 210121.455C9

CURRENT APPLICANT: ON NUMBER: US/09/606,421B

CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SOFTWARE: PRETENCE FRETSEC for Windows Version 3.0
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COTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapien
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US-09-606-421B-105
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\begin{array}{c} 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\
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  Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2 1/USFTO spool p/US10039272/runat 07092004 144222 21609/app query.fasta_1.2823
-DB=A_Geneseq_29ānu04 -QFNT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPGE=0
-LOOPEXH=0 -UNITS=bits -CFNT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPGE=0
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-UNITS=bits -CFNT=Fasta -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-UNDE-LOCAL -OUTFWH=pto -NORH=ext -HEADSIZE=500 -MINIEN=0 -MAXIEN=2000000000
-USER=USI0039272 @CGN_1 1_265 @runat 0709204 144222_21609 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMBOUT=120 -WARN_IMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Aab11329 Human lun
Abb78200 Amino aci
Abb74961 Human lun
Abb6592 Lung canc
Abd72962 Human ost
Abd72962 Human ost
Abd782815 Human adi
Add28315 Human lun
Add78235 Human CGD
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(without alignments)
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                 frame_plus_n2p model
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ABB78200
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ABP61881
ABU56592
ABU70852
ADD78335
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Maximum Match 100%
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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Result Š.

Mouse Urogenital Sinus (UGS) tissue was isolated from 17 day old mouse embryos. The UGS cells were infected with retroviruses, cultured and implanted under the renal capsule of mice. Reconstitutions were harvested 5 weeks later, when they showed signs of distress from the tumour burden. Metastasised tumours were isolated from a site outside the renal capsule. RNA was isolated from primary tumours and metastases, reverse transcribed and subjected to differential display PCR. The sequences were analysed to obtain metastatic sequences e.g. the sequence encoding the present sequence. The method can be used to detect, diagnose and treat disorders related to metastasis, or treat malignant or non-malignant disorders, e.g. hyperplasia, dysplasia and hypertrophy. The metastatic sequence can be used to screen a biological sample for metastasis, and it or its expression product may also be used to treat a metastatic disorder Disclosure, Fig 12CI; 102pp; English. 

Sequence 560 AA;

Alignment Sc Pred. No.: Score: Percent Sim. Best Local ( Query Match DB:	t Scores: : Similarity: al Similarity: tch:	4.82e-295 2999.00 99.82% 99.82% 1.84%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	560 0 1 1 0
US-10-03	9-272-1 (1-266	1) x AAW35382 (1	-560)	
λo	60 ATGGAATGTCTCTA	CTATTC	CTGGGATTTCTGCTCCTGG	SCTGCAAGATTGCCACTTGAT 119
qa	1 MetGluCy	sleufyrfyrPheleu	sLeuTyrTyrPheLeuGlyPheLeuLeuLeuA	
δλ	120 GCCGCCAAAC	SATTTCA	CTGGGCAATGAAAGAC	CCTTCTGCTTACATGAGGGAG 179
쉽	laAl	sArgPheHisAspVal	LeuGlyAsnGluArgF	roSerAlaTyrMe
ò	180 CACAATCA	ATTAAATGGCTGGTCT	TCTGATGAAAATGACT	CAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAAAAAGCTCTACCCA 239
qa	41 HisAsnGl		SerAspGluAsnAspT	
δ	240 GTGTGGAA	GCGGGGAGACATGAGG	TGGAAAACTCCTGGA	GTGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAGGCGTGTGCAGGCG 299
q <sub>0</sub>	61 ValTrpLy	sArgGlyAspMetArg	TrpLysAsnSerTrpL	ysglyglyArgValGlnAla 80
δλ	300 GTCCTGAC	CCAGTGACTCACCAGCC	CTCGTGGGCTCAAATA	ATAACATTTGCGGTGAACCTG 359
Db		rSerAspSerProAla	LeuValGlySerAsnl	LeuThrSerAspSerProAlaLeuValGlySerAsnIleThrPheAlaValAsnLeu 100
ζŏ	360 ATATTCCC	TAGATGCCAAAAGGAA	GATGCCAATGGCAACA	ATATTCCCTAGATGCCAAAAGGAAGGTGCCAATGGCAACATAGTCTATGAGAAGAACTGC 419
qq	101 IlePhePr	oArgCysGlnLysGlu	PheProArgCysGlnLysGluAspAlaAsnGlyAsnI	
ζ	420 AGAAATGA	GGCTGGTTTATCTGCT	GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGC	AACTGGACAGCATGGTCAGAG 479
Ор	121 ArgAsnGl	uAlaGlyLeuSerAla	AspProTyrValTyrA	
ò	480 GACAGTGA	CGGGGAAAATGGCACC	GGCCAAAGCCATCATA	GACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAA 539
QO	141 ABDSerAB	pGlyGluAsnGlyThr	GlyGlnSerHisHisA	AsnValPheProAspGlyLys 160
ò	540 CCTTTTCC	TCACCACCCGGATGG	CCTTTTCCTCACCCCGGATGGAGAAGATGGAATTTCAT	ATCTACGTCTTCCACACATT 599
QΩ	161 ProPheProH	oHisHisProGlyTrp	ProGlyTrpArgArgTrpAsnPhell	
ò	600 GGTCAGTATTTC	TTTCCAGAAATTGGGACGATGTT	ACGATGTTCAGTGAGAC	TCTGTGAACACAG
QQ	181 GlyGlnTy	rPheGlnLysLeuGly	GlyGlnTyrPheGlnLysLeuGlyArgCysSerValArgVal	/alservalasnThralaasn 200
λ	660 GTGACACT	TGGGCCTCAACTCATG	SGAAGTGACTGTCTACA	TGACACTIGGGCCTCAACTCAIGGAAGTGACTGTCTACAGAAGACATGGACGGGCATAT 719
ДD	201 ValThrLe	uGlyProGlnLeuMet	GluValThrValTyr	ArgarghisGlyArgalaTyr 220
۵,	720 GTTCCCA1	CCCCACAAGTGAAAGAT	rgtgtacgtggtaacac	GTTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTG 779

Db 221	
780	ACTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCC-AAAGATCTCCCC 838
839	ATTANGTITGANGTCCTGANTCANGANCCTAGCCACTITCCTCCATTANTCTACCATTAAC 898
899	TACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTT
5	ACGIAIGIGCTCAATGGAACCTTCAGCCTTAACCTCACTGAGAAGCTGCAGC
Db 301	
Oy 1019	GGACCTIGICCGCCACCGCCACCACCACGACCCTTCAAAACCCACCCCTTTTAGGA 1078
Oy 1079	CCTGCTGGTGACAACCCCCTGGAGCTGAGATAGGATTCCTGATGAAAACTGCCAGATTAAC 1138
113	GATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATC 11
Db 361	rgfyrGlyhisPhedinAlaThrileThrilevalGluGlyllebeuGluvalAbnil nrcagangaCagarGTCCTGATGCCGGTGCCATGGCCTGAAAGGTCCCTAATAGATT
388	
Oy 1259	GTGGTGACCTGCCCAGGGGGGTCTGGACCATGGTTTCTGACCCCACC 1318
. 13	GCGAGATCACCCAGAACACACTGTGCAGCCCTGTGGATGTGTGAGATGTGTTGTCTGCTG 13
Db 421	sGluileThrGlinAsnThrValCysSerProValAspValAspGluMetCysLeuLeu 44
Oy 1379 Db 441	ACTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGAACCTCACCCTGGGGGGT 1438 
Qy 1439	ACACAAGCCTGGCTCTCACCTCACCTGATTTCTGTTTCTGACAGACCCAGCCT
Db 461	
149	GTCACT 15
Db 481	roLeuArgMetAlaAsnSerAlaLeuIleSerValGlyCysLeuAlallePheValThr 500
Qy 1559 Db 501	GTGATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCT 1618 
2y 1619	GGAATGTGGTCAGAAGCGCCTGAGTCTTTCTCAACGCGTGTTT
Db 521	
2y 1679	TCCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCT 17.
Db 541	eProGlyAsnGlnGluLysAspProLeuLeuLysAsnGlnGluPheLysGlyValS
RESULT 2 AABI1329 ID AABI1329 XX AC AABI1329	standard; protein; 560 AA.

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CACACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCA 1018
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                                                                               IlePheProArgCysGlnLysGluAspAlaAsnGlyAsnIleValTyrGluLysAsnCys
                                                                                                                                   ProPheProHishisProGlyTrpArgArgTrpAsnPheIleTyrValPheHisThrLeu
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     GTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTG
                                                            ATATICCCTAGAIGCCAAAAAGGAAGAIGCCAAIGGCAACAIAGICTAIGAGAAGAACIGC
                                                                                                                   AGAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel isolated polypeptide (I) which comparising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polymoleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient est tracted with P2, polymucleotides encoding P2 or antigen presenting development of cancer
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                                                      er; therapy; treatment; human; tumor; immunogenic; cytostatic; detection.
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                          Human lung cancer-associated protein L528S
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neurokin-1 type (HGFIN) polypeptide. HGFIN induces white blood cell differentiation and inhibits progenitor proliferation. HGFIN polypeptides and polymucleotides are useful for treating a disease associated with abnormal bone marrow cell differentiation or proliferation, especially acute myeloid leukemia, acute lymphocytic leukemia, chronic myeloid leukemia, leukemia, hodgkin's and non-Hodgkin's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present sequence represents haematopoietic growth factor inducible
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                                                                                                                                                                                                                                                      GlyAsnValValArgSerLy8GlyLeuSerValPheLeuAsnArgAlaLysAlaValPhe
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        ThrvalArgArgThrPheAsnGlySerGlyThrTyrCysValAsnLeuThrLeuGlyAsp
                                                                                               AspThrSerLeuAlaLeuThrSerThrLeuIleSerValProAspArgAspProAlaSer
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                                                                      GACACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTT
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N-PSDB; ABQ78551.
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comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung acncer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                             The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions
                                                                                                                                                                                                                 Polynucleotides encoding lung tumor polypeptides, lung cancer or stimulating an immune response.
                                                                                                                                                                                                                                           Disclosure; Page 281-283; 374pp; English.
                                                                  28-JUN-2000; 2000US-00666421.
02-AUG-2000; 2000US-00630940.
11-SEP-2000; 2000US-00663787.
15-SEP-2000; 2000US-00662786.
09-OCT-2000; 2000US-00685696.
12-DEC-2000; 2000US-00735705.
07-MAY-2001; 2001US-00850716.
                                                                                                                                          (CORI-) CORIXA CORP.
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Henderson Ri Fanger GR;

/ YAW, Li SX, Kalos MD, F Retter MW, Marnerakis M, Watanabe Y, Peckham DW;

ng A, Skeiky YAW, Fanger N, Retter Carter D, Watana

2001WO-US021065

ATGGAATGTCTCTACTATTTCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGAT 119 179 239 299 359 100 419 120 40 09 80 GCCGCCAAACGATTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAG CACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAACTCTACCCA GTGTGGAAGCGGGAACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCG GTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAAACATTTGCGGTGAACCTG 81 ValLeuThrSerAspSerProAlaLeuValGlySerAsnlleThrPheAlaValAsnLeu ATATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGC 560 559 0 1 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-10-039-272-1 (1-2661) x ABB74961 (1-560) 4.82e-295 2999.00 99.82% 99.82% Percent Similarity: Best Local Similarity: Alignment Scores: 41 240 61 300 360 ద d à ð 9 Pb  $\overset{\circ}{\circ}$ 

lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

immune response

Human;

sapiens

Homo

SEQ ID NO:225

tumour L528S protein sequence

(first

01-MAY-2002 Human lung

ABB74961

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ABB74961 standard; protein;

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                                              221 ValProileAlaGinValLysAspValTyrValValThrAspGinileProValPheVal
                CCTITITCCTCACCACCCCGGATGGAAGATGGAATTTCATCTACGTCTTCCACACACTT
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The present invention describes isolated human lung carcinoma computation describes isolated human lung carcinoma delivity, and can be used in gene therapy and in vaccines. Compositions activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonuclectides of containing a biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample with the oligonuclectide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to
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                               GTGATCTCCCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCT
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the polynucleotides, useful in pharmaceutical compositions such
vaccines and as markers to indicate the presence of lung cancer.
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PD, Fanger N, Retter MW, Durham M, Fanger GR,
J, Watanabe Y, Peckham DW, Cai F, Foy TM;
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07-MAX-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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1019 GGACCTTGTCCGCCA 	1139 AGATATGGCCACT 	1199 ATCCAC          381 IleGlr	1259 GTCGTGACCTGC              401 ValValThrCys	Qy 1319 TGCGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGAGATGTGTGTG	Qy 1379 ACTGTGAGGCGAACCTTCAATGGGTCTGGGGACGTACTGTGAACCTCACCCTGGGGGGT 1438	Oy 1439 GACACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCG 1498	Qy 1499 CCTTTAAGGATGGCAAACAGTGCCCTGGTTGGCTTGGCCATATTTGTCACT 1558	Qy 1559 GTGATCTCCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAATAGAAATAGTCT 1618	QY 1619 GGGAATGTGGTCAGAAGCCAGAGTGTCTTTCTCAACCGTGCAAAAGCCGTGTTC 1678	QY 1679 TTCCGGGAAAACCGGATCGCTACTCAAAAACCAGAATTTAAAGGAGTTTCT 1738	RESULT 6 ABUS6592 ID ABUS6592 standard; protein; 560 AA. XX	AC ABUS6592; XX XX 02-APR-2003 (first entry)	ng cancer-associated polypeptide #185.  ng cancer-associated polypeptide; cytostatic; emphysema;	KW small cell lung cancer; benign lesion; precancercus lesion; bronchitis; KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis; KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis. XX	OS Unidentified. XX PN W0200286443-A2.	AA PD 31-OCT-2002. XX PF 18-APR-2002; 2002WO-US012476.
Alignment Scores:  Pred. No.: Score: Score: Score: Percent Similarity: 99.82\$ Mismatches: Best Local Similarity: 99.82\$ Mismatches: 1 Query Match: 61.84\$ Indels: 1 US-10-039-272-1 (1-2661) x ABP61881 (1-560)	Qy 60 AIGGAAIGTCICTACIAITICCIGGAAITICIGCICCIGGAGGAIGATGCCACTIGAI 119	Qy 120 GCCGCCAAACGATTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGG 179	OY 180 CACAATCAATTAAATGGCTGGTCTTCTGATGAAAAGGTGGGAATGAAAAACTCTACCCA 239 	OY 240 GTGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGGGGGG	OY 300 GTCCTGACCAGGCCTCGAGCCTCGAGATATATAACATTTGCGGTGAACCTG 359	Qy 360 ATATTCCTAGATGCCAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGC 419	3 47	8=2	TCCTCACCACCCCGGATGGAGATGGAATTTCATCTACGTCTTCCACACACTT		OY 660 GTGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATAT 719	TTGTG 77	CCCC 83	TAAC       eAsn	GAAT 95	59 CACACGTAITGCTCAATGGAACCTTCAGCCTTAACCTCATGTGAAAGCTGCAGCACCA 10

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; 2001US-0284770P.
; 2001US-0290492P.
; 2001US-033245P.
; 2001US-033666P.
; 2002US-0334370P.
                               (EOSB-) EOS BIOTECHNOLOGY INC
                                               WPI; 2003-093161/08.
N-PSDB; ABX76321.
                                        Murray R;
18-APR-2001; 2
10-MAY-2001; 2
09-NOV-2001; 3
             13-NOV-2001;
29-NOV-2001;
12-APR-2002;
                                       Aziz N,
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Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.

Claim 27; Page 328; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynuclectide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynuclectides and polypeptides are used for identifying a compound that medulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensativity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodises. Sequences ABU56048-ABU56745 represent lung cancer-associated polypeptides of the

Sequence 560 AA;

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Length:	Macches: Conservative:	Mismatches: Indels:	Gaps:
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US-10-039-272-1 (1-2661) x ABUS6592 (1-560)

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120	120 GCCGCCAAACGATTICATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAG 179	179
21	21 AlaAlaLysArgPheHisAspValLeuGlyAsnGluArgProSerAlaTyrMetArgGlu 40	40
180	180 CACAATCAATTAAATGGCTGGTCTTCTGATGAAAAAGACTGGAATGAAAAAAACCCCA 239	239
41	41 HisasnGluLeuasnGlyTrpSerSerAspGluAsnAspTrpAsnGluLysLeuTyrPro 60	09
240	240 GTGTGGAAGCGGGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCC 299	299
61	61 ValTrpLysArgGlyAspMetArgTrpLysAsnSerTrpLysGlyGlyArgValGlnAla 80	80
300	GTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAAACATTTGCGGTGAACCTG 359	359
81	81 ValleuThrSerAspSerProAlaLeuValGlySerAsnIleThrPheAlaValAsnLeu	100

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QQ	201	valThrLeuGlyProGinLeuMetGiuValinrvaliyrArgArghibGiyArgAraiyi 220
OY DP	720 (	STTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTG 779 
<i>ك</i> ر	780	ACTATOTICCAGAAGAACGATCGAAATICATCGACGAAACCTTCCC-AAAGATCTCCC 838
Db	241	
δ	839	MITATGITIGAGGICCIGATICATGATCCTAGCCACTICCTCAATTATICTACCATTAAC 898
QΩ	261	IleMetPheAspValLeulleHisAspProSerHisPheLeuAsnTyrSerThrileAsn 280
٥٨	899	IRCAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATCGTGAAT 958
qq	281	IyrLysTrpSerPheGlyAspAsnThrGlyLeuPheValSerThrAsnHisThrValAsn 300
δÿ	959	CACACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCA 1018
qa	301	HisthriyrValLeuAsnclythrPheSerLeuAsnLeuThrValLysAlaAlaAlaPro 320
δ	1019	
Dp	321	GlyProCysProProProProProProArgProSerLysProThrProSerLeuGly 340
ò	1079	CCTGCTGGTGACAACCCCCTGGAGCTGAGTAGGATTCCTGATGAAAACTGCCAGATTAAC 1138
qq	341	ProAlaGlyAspAsnProLeuGluLeuSerArgIleProAspGluAsnCysGlnIleAsn 360
\dot \dot \dot \dot \dot \dot \dot \dot	1139	AGATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATC 1198
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λ 4.	1259	GTGGTGACCTGCCAAGGGAGCATTCCCAGGAGGTCTGTACCATATTTGTGACCCCACC 1318
3	H	0000 CECUECECECECECECECECECECECECECECECECECE
중 음	1319	TGCGAGATCACCCAGAACAAGTCTGCAGGCCTGTGGATGTGGATGATGATGTGGTGTGTGT
Š	1379	actericaga certica a mesegnicines acenaemes a 1438
<b>3</b> 43	441	
λŏ	1439	GACACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCG 1498

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The invention describes an isolated and substantially pure osteoactivin protein (1) that stimulates bone cell differentiation. A therapeutic composition comprising (1), the polynuclectide (1) encoding (1) or a biologically active fragment of (1) is useful for trimulating bone formation in a mammal. The composition is also useful for treating a bone disorder including osteoporosis and periodontal disease. A second therapeutic composition comprsising an anti-(1) antibody or an agent that inhibits osteoactivin-mediated bone formation is useful for inhibiting formation in a mammal. The second composition is also useful for treating correction in a mammal. The second composition is also useful for treating for developing novel therapeutic compositions for bone disorders, and for stimulating osteogenesis. The polynucleotide is also useful in gene therapy. This is the amino acid sequence of human nmb, a homologue of the rat osteoactivin of the invention used in the creation of antibodies for
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bone disorders
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; osteoactivin; osteopathic; antiinflammatory; vaccine;
bone cell differentiation stumulator; gene therapy; bone formation;
osteoporosis; periodontal disease; ectopic bone formation; osteopetrosis;
bone disorder; osteogenesis; enzyme.
GTGATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCT
                                                                                                                                                                                  PhebroglyAsnGlnGluLysAspProLeuLeuLysAsnGlnGluPheLysGlyValSer
                                              CCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTTGGCTTGGCCATATTTGTCACT
                                                                                                                          GGGAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACGGTGCAAAAGCCGTGTTC
                                                                                                                                                                                                                          TTCCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAAGGAGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated osteoactivin protein and gene encoding for stimulating bone differentiation and for treating including osteoporosis and periodontal disease.
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                                                                                                                                                                                                                                                                                                                                                                                                        Human osteoactivin homologue, nmb.
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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified composite and known adipocyte marker and then by selecting a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by performing a generating domains) proteins. Also included are a polymucleotide encoding a polypeptide in the adipocyte cells, a compinant host cell expressing at least one of the interacting recombinant host cell expressing at least one of the interacting compound in adipocyte cells, a sID (RTM) polypeptide comprising any of the 738 amino acid comprising the specification (including its fragment or variant), a squences given in the specification (including its fragment or variant), a vector comprising the vector, a protein chip comprising the polypeptides and a recombinant host cell comprising the vector, a protein chip comprising the polypeptides and a compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polymucleotides are useful as probes or primers. The complex is preventing or treating metabolic disorders such as obesity or diabetes. The polymucleotides are useful as probes or primers. The complex is comprising the therapeutic effect. The present sequence represents a SID (RTM) protein of the invention
                                                                                                                                                                                                 New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
                                                                                                                                                                                                                                                                                                                    Claim 6; Page 269-270; 382pp; English.
                                         14-MAR-2001; 2001US-0275734P.
14-MAR-2002; 2002WO-EP003768
                                                                                                                                                              WPI; 2003-103412/09.
                                                                                                                     Legrain P, Daviet
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                                             381 IleGlnMetThrAspValLeuMetProValProTrpProGluSerSerLeuIleAspPhe
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21 AlaAlaLySArgPheHiSAspValLeuGlyAsnGluArgProSerAlaTyrMetArgGlu 41 HisasnGlnLeuasnGlyTrpSerSeraspGluasnaspTrpAsnGluLysLeuTyrPro ATGGAATGTCTCTACTATTTCCTGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGAT 1 MetGluCysLeuTyrTyrPheLeuGlyPheLeuLeuAlaAlaArgLeuProLeuAsp 120 GCCGCCAAACGATTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAG CACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAACTCTACCCA GTGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCG 560 0 1 1 Conservative: Mismatches: Indels: Length: Matches: Gaps: US-10-039-272-1 (1-2661) x ABU70852 (1-560) 4.82e-295 2999.00 99.82% 99.82% Best Local Similarity: Percent Similarity: 09 180 240 61 Query Match: DB: ð 셤 d ð 셤 ð d ð

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GTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTG

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prey; adipocyte; SID; selected interacting domain; anorectic; betic; protein-protein interaction; diabetes; .hybrid assay; metabolic disorder; obesity.

yeast 2-hybrid

Homo

WO200286122-A2. 31-OCT-2002

Human adipocyte Selected Interacting domain, SID, #483

(first entry)

10-JUN-2003

ABU70852;

ABU70852 standard; protein; 560 AA.

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Qy         1439 GACACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCG 1498           Db         461 AspThrSerLeualaLeuThrSerThrLeuIlSerValPrOAspArgAspProAlaSer 480           Qy         1499 CCTTTAAGGATGGCAAACAGTGCCTGATCTCGTTGGCTGCTTGGCCATATTGTCACT 1558           Db         481 ProLeuargMetAlaAsnSerAlaLeuIlSeSerValGlyCysLeualaIlSeheValThr 500           Qy         1559 GTGATCTCCTCTTGGTGTACAAAAAACACAAGGAATACAACCCAATAGAAAATAGTCT 1618           Db         501 ValIlSeSerLeuLeuValTyrLysLysHisLysGluTyrAsnProIlGGluAsnSerPro 520           Qy         1619 GGGAATGGGTCAGAAGGCCTGAGTGCTTTCTCAACCGTGCAAAAGCCGTGCTTC 1678           Db         521 GIyAsnValValArgSerLysGlyLeuSerValPheLeuAsnArgAlaValPhe 540           Qy         1679 TTCCCGGGAAACCAGGAAAGGATCCGTACTCTTTCTCAACGTGCAAAAGCAGTTTCT 1738           Qy         1679 TTCCCGGGAAACCAGGAAAGGATCCGTACAAAAACCAAGAATTTAAAGGAGTTTCT 1738           Db         541 PheProGlyAsnGloluysAsnGlnGluGhelvsAsnGlnGluGhelvsGlvAalSer 560	VULT 9 128315 ADA28315; ADA28315; 20-NOV-2003 (first entry) Human lung tumour L528S protein. cancer; lung cancer; gene therapy; vaccine; human; lung squamous cell carcinoma. Homo sapiens.	PN US2003064947-A1.  PN US2003064947-A1.  PD 03-APR-2003.  XX  PF 30-NOV-2001; 2001US-00007700.  XX  PR 18-MAR-1998; 99US-00123912.  PR 22-DEC-1998; 99US-00123912.  PR 22-DEC-1998; 99US-00285479.  PR 17-DEC-1999; 99US-00466396.  PR 30-DEC-1999; 99US-0048084.  PR 10-JAN-2000; 2000US-0048084.  PR 04-APR-2000; 2000US-00510376.  PR 04-APR-2000; 2000US-00606421.  PR 02-DEC-2000; 2000US-00606421.  PR 22-DUN-2000; 2000US-00606421.  PR 22-DUN-2000; 2000US-00606421.  PR 22-AUG-2000; 2000US-0063940.  PR 15-SEP-2000; 2000US-00662786.	09-OCT-2000; 07-MAX-2001; 28-JUN-2001; 28-JUN-2001; (CORI-) CORI Wang T, Wan Mcneill PD, Carter D, W WPI; 2003-54 New isolated preventing a Example 7; P
0 ATATTCCCTAGATGCCAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGC 1	0 GTGACACTTGGGCCTCAACTCATGGAAGTGACTCTACAGAAGACATGGACGGCCATAT 71	9 TACAAGTGGAGCTTGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGT 9 TACAAGTGGAGCTTGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGT 1	361 ArgTyrClyHisPheGlnAlaThrill

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for diagnosing, preventing and/or treating cancer, particularly lung defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; at sequence that hybridise to any of the nucleotide sequences cited above; a stringent conditions; a sequence that is at least 75 or 90% identical to the above nucleotide sequences; or degenerate variants of the above nucleotide sequence; or degenerate variants of the above nucleotide sequences. The composition and methods are useful in gene therapy and in vaccines. This is the amino acid sequence encoded by a human lung tumour cDNA isolated from a lung squamous cell carcinoma that may be useful in the diagnosis and treatment of lung cancer and
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Anabolic, Hypertensive; Respiratory; Anti-HIV; Antiallergic, Neuroprotective; Nootropic, Antianemic; Antiarteriosclerotic; Antiinflammacry; Opthalmological; Muscular; Hepatotropic; Neuroprotective; Antiasthmatic; Anticonvulsant; Virucide; Antibacterial; Fungicide; Antiparasitic; Anticonvulsant; Virucide; Antibacterial; Cerebroprotective; Antiparkinsonian; Antipsoriatic; Antigout; Antidabetic; Antiric; Antirheumatic; Osteopathic; Gene therapy; Antidiabetic; Antiarthritic; Antirheumatic; Osteopathic; Gene therapy; cell proliferative disorder; cancer; developmental disorder; enterior, official differential disorder; inflammatory disorder; informatic; official disorder; inflammatory disorder;
                                                                                                                                       infection; reproductive disorder.
                                                                                                                                                                                                                                        15-MAR-2002; 2002US-0364494P.
29-MAR-2002; 2002US-0369129P.
12-APR-2002; 2002US-0372511P.
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Elliott VS, our...
-ha SD, Lee SY, Swar...
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         Human CGDD-16
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Kable AE, Tran UK, Hafalia AJA, Burford N, Honchell CD, Lehr-Mason PM, Duggan BM, Ramkumar J, Griffin JA, Richardson TW; Elliott VS, Jiang X, Jackson AA, Marquis JP, Chawla NK, Khare R; Becha SD, Lee SY, Swarnaka A, Yue H, Warren BA, Baughn MR, Lal PG; Lee S, Ho A, Gandhi AR, Xao MG;

WPI; 2003-779081/73. N-PSDB; ADD78274.

New polypeptides and polynucleotides associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing e.g. developmental, neurological, autoimmune, inflammatory or reproductive disorders.

Claim 1; SEQ ID NO 16; 320pp; English.

The present invention relates to novel human proteins (1; ADD78220-ADD78258) and their coding sequences (II; ADD78259-ADD78297), which are associated with cell growth, differentiation and death, referred to as CGDD-n proteins, where n is a number from 1 to 39. The CGDD proteins and their coding sequences are useful for diagnosing, treating or preventing cell proliferative disorders (e.g. cirrhosis, hepatitis, arences or cancers (e.g. cirrhosis, bone marrow, brain, breast, colon, kidney, liver, lung or uterus), developmental disorders of e.g. renal tubular acidosis, Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism or saizures), neurological disorders (e.g. pick's disease, cataract, epilepsy, ischemic cerebrovascular disease, autoimmune/inflammatory disorders (e.g. Albs, allergies, anemia, asthma, autoimmune/inflammatory disorders (e.g. Albs, allergies, anemia, asthma, diabetes mellitus, bronchitis, osteoprosis, osteoarthritis, rheumatoid arthritis, contact demantitis or gout), viral, bacterial, fungal, parastic, protozoan or helminthic infections, reproductive disorders (e.g. infertility, ectopic pregnancy, premature ovarian failure, delayed choriccarcinoma, placenta previa, placental cor maternal floor infarction or chronic villitis).

Sequence 572 AA;

Length: Matches: Conservative: 4.16e-293 2980.00 97.73% Percent Similarity: Alignment Scores: Pred. No.: Score:

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                                                                                                                                                                                           CysSerProvalAspValAspGluMetCysLeuLeuThrValArgArgThrPheAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
breast cancer; prostate tumour; rectal tumour; liver tumour;
pericyte cell proliferation; chondrocyte cell proliferation;
tumour necrosis factor-alpha.
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29-JUN-2001; 2001WO-US021066. 20-JUL-2000; 2000US-0219556P.

31-JAN-2002.

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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, tumour. Dreast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in perioyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human blood, for stimulating or inhibiting the proliferation of normal human blood, fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue tryping. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AMU83592-AAU83713 represent human PRO protein sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGAATGTCTCTACTATTTCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGAT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetGluCysLeuTyrTyrPheLeuGlyPheLeuLeuLeuAlaAlaArgLeuProLeuAsp
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Smith V, Stephan JF, Watanabe CK,
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Matches:
Conservative:
Mismatches:
Indels:
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2000US-0220607P
2000US-0220607P
2000US-0220634P
2000US-0220664P
2000US-0220664P
2000US-0220863P
2000US-0220893P
2000US-0220893P
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2000US-0253646P.
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2000US-00747259.
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28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
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10-MAY-2001; 2001US-00854208
10-MAY-2001; 2001US-00854280
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2000WO-US023328.
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AĽ,
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C, Gurney
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N-PSDB; ABK33556.
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Best Local Similarity:
Query Match:
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    25-JUL-2000; 25-JUL-2000; 25-JUL-2000; 25-JUL-2000; 25-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 20-JUL-2000; 20-JU
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One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating tumor.

Claim 11; Fig 42; 314pp; English.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABUS0739-ABUS0860 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence USPTO web site at sequence USPTO web site at sequence.

Sequence 572 AA;

		119	20	179	40	239	09	299	80	359	100	419	120	479	140	539	160	599	180	629	200
26e-293 Length: 572 79.00 Matches: 558 .55\$ Conservative: 0 .55\$ Mismatches: 2 .42\$ Indels: 13	x ABU80759 (1-572)	ATGGAATGTCTCTACTATTTCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGAT 115	MetGluCysLeuTyrTyrPheLeuGlyPheLeuLeuAlaAlaArgLeuProLeuAsp 20	17	AlaAlaLysArgPheHisAspValLeuGlyAsnGluArgProSerAlaTyrMetArgGlu 40	CACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAACTCTACCCA 239	9	σ	80	D.	10	41	12	7	14	53	AspSerAspGlyGluAsnGlyThrGlyGlnSerHisHisAsnValPheProAspGlyLys 16	T 59	18	GGTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAAT 65:	GlyGlnTyrPheGlnLysLeuGlyArgCysSerValArgValSerValAsnThrAlaAsn 20
5. 297 ty: 97 61	(1-2661)	ATGGAATGTCTC	MetGluCysLeu	GCGCCAAACGA	AlaAlaLysArg	CACAATCAATTA	HisAsnGlnLeu	GTGTGGAAGCGG	riiiii ValTrpLysArg	GTCCTGACCAGT	ValLeuThrSer	ATATTCCCTAGA	llePheProArg	AGAAATGAGGCT	ArgAsnGluAla ArgAsnGluAla	GACAGTGACGGG	AspSerAspGly	CCTTTTCCTCAC	ProPheProHis	GGTCAGTATTTC	GlyGlnTyrPhe
Scores milari Simil h:	-272-1	09	7	120	21 /	180	41 F	240 (	61	300 (	81	360 7	101	420 /	121	480 (	141	540	161	009	181
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201 ValThrLeuGlyProGlnLeuMetGluValThrValTyrArgArgHisGlyArgAlaTyr 220

GTGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATAT

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δy	720	GTTCCCATCGCACAAGTGAAAGATGTGCTACGGAAACAGATCCAGATTCCTGTGTTTGTG 779
ΩĐ	221	ValProlleAlaGlnValLysAspValTyrValValThrAspGln1leProValPheVal 240
δγ	780	ACTAINGTICCAGAAGAACGAICGAATTCAITCAGAGAACTTCCC-AAAGAICTCCCC 838
QQ	241	ThrMetPheGlnLysAsnAspArgAsnSerSerAspGluThrPheLeuLysAspLeuPro 260
۲۵ s	839	839 ATTAIGNIGATICAIGATICAIGAICCTAGCCACTICCTCAATTAITCTACCATTAAC 898
Ωp	261	<pre>IleMetPheAspValLeulleHisAspProSerHisPheLeuAsnTyrSerThrIleAsn 280</pre>
à	899	TACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTT
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ð í	959	CACACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCA 1018
gn	TO F	
දු ද	1019	GGACCTTGTCGCCACCGCCACCACCACCACCACCATCAAACCCACCC
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Š :	107	
Ωρ	341	
δλ	1103	CTGAGTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACC 1162
Dp	361	LeuSerArglleProAspGluAsnCysGlnIleAsnArgTyrGlyHisPheGlnAlaThr 380
٥٧	1163	ATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGCCCTGATG 1222
Db	381	ileThrileValGluGlyileLeuGluValAsnileileGlnMetThrAspValLeuMet 400
δλ	1223	CCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGGGGGCATT 1282
qq	401	ProvalProTrpProGluSerSerLeuIleAspPheValValThrCysGlnGlySerIle 420
δ	1283	CCCACGGAGGTCTGTACCATCATTTCTGACCCCACTGCGAGATCACCCAGAACACAGTC 1342
qa	421	ProThrGluValCysThrIleIleSerAspProThrCysGluIleThrGlnAsnThrVal 440
à	1343	TGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAGACGAACGA
qq	441	CysserProValAspValAspGluMetCysLeuLeuThrValArgArgThrPheAsnGly 460
δχ	1403	TCTGGGACGTACTGTGTGACCTCACCCTGGGGGATGACACAAGCCTGGCTCTCACGAGC 1462
Db	461	SerGlyThrTyrCysValAsnLeuThrLeuGlyAspAspThrSerLeuAlaLeuThrSer 480
o VO	1463	ACCCIGATITICIGITICTGACAGAGACCCAGCCTTGCCTT
qq	481	ThrLeulleSerValProAspArgAspProAlaSerProLeuArgMetAlaAsnSerAla 500
ζ	1523	CTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAA 1582
o QQ	501	LeuileSerValGlyCysLeuAlailePheValThrValileSerLeuLeuValTyrLys 520
ò	1583	AAACACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGC 1642
q <sub>O</sub>	521	
ò	1643	CTGAGTGTCTTTCTCAACCGTCCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGAT 1702
Db	541	LeuserValphereuAsnArgAlaIysAlaValPhePheProGlyAsnGlnGluLysAsp 560
δλ	1703	CCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCT 1738
qq	561	ProLeuLysAsnGinGluPheLysGlyValSer 572

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antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; pericyte stimulator; fibroblast modulator; pharmaceutical; diagnostic; biosensor; bioreactor; tumnour; hung tumnor; colon tumnour; breast tumnour; prostate tumnour; rectal tumnour; liver tumnour; bone disorder; cartilage disorder; sports injury;
                                                                                                                                                                                                                                                                                   Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                      transmembrane protein; PRO; cytostatic;
                                                                    Novel human secreted and transmembrane protein PRO9925.
               AB033725 standard; protein; 572 AA.
                                                                                                                                                                                                             12-AUG-2002; 2002US-00218631.
                                                                                                                                                                                                                              01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                   (first entry)
                                                                                                                                                                                                                                                                                  Desnoyers L,
                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                      secreted and
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N-PSDB; ACD68613.
                                                                                                                                          arthritis; wound
                                                                                                                                                                           US2003045687-A1.
                                                                                                                                                                                                                                                                                          Grimaldi JC,
                                                                                                                                                          Homo sapiens.
                                                   17-SEP-2003
                                                                                                                                                                                            06-MAR-2003
                                 AB033725;
                                                                                                                                                                                                                                                                                  Baker KP,
RESULT 13
         AB033725
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New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or wounds in a mammal.

Claim 11; Fig 42; 314pp; English.

The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting tumour, colon tumour, breast tumour, prostate tumour, secral tumour, or liver tumour) or timulating the proliferation of differentiation of chondrocyte for stimulating proliferation of inferentiation of chondrocyte cells, for stimulating proliferation of pericyte cells, or for modulating nor polypeptide is also useful for treating tumours or various bone and/or cartilage disorders (e.g. sports injuries or articularly as targets or PRO polypeptides are useful in drug screening, particularly as targets of the their petul cintervention in these diseases, and in the diagnostic or Arearing the properties of the properties of the properties of the properties of the process of the process of the properties of the process of determination of the presence of these diseases. The PRO polyptides are also useful as molecular weight markers, or for chromosome lidentification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide

Sequence 572 AA;

Alignment Pred. No. Score: Percent & Best Loce Query Mat DB:	t Scores: .: Similarit al Simila	y: rity:	5.26 2979 97.59 97.56	0	Length: Matches: Conservative: Mismatches: Indels:	572 558 0 2 1 1		
US-10-039	9-272-1 (	1-2661	X A	BO33725	(1-572)			
Qy Db	60 ATG     1 Met	ATGGAATGT            MetGluCys	CTCTACTAT           LeuTyrTyr	TTCC	TGGGATTTCTGCTCCT	GGCTGC        uAlaAl	AAGATTGCCACTTGA                         aArgLeuProLeuAsj	T 119   P 20
Ολ	120 GCCG	GCCAAA	CGATT	ATG	GCTGGGCAATGAAAG	H-	CATGAGGG	G 179
Ор	21 Ala	AlaLys		_ds.		to		
දු දු	180 CAC 	CAATCAAT	TTAAA:       LeuAsi	TTAAATGGCTGGTC              LeuAsnGlyTrpSe	CTTCTGATGAAAATGAC 	CTGGAATGAAAAAC 	AAAAACTCTACCCA	A 239
λό qa	240 GTGTG      61 ValT	GGAAC	GCGGGGAGACAT 	_g=;;	GTGGAAAAACTCCT 	- <u></u> -	TGCAGG	Ω — α 22 — α
ò	300 GTC	IGAC(	AGTGA	ACCAC	- 5	TATAACAT	GCGGT	359
qa	81 Vall		SerAsi	rPro				- 7
Vy Dp	360 ATAT7	55 — g	AGATGO	CTAGATGCCAAAAGGAAGATGC                   roArqCysGlnLysGluAspAl	AGATGCCAATGGCAACAT	CATAGICIAIC	ATGAGAAGAACTGC	C 419
ò	420 AGA	AATGAG	SCTGG	TTATCTGC	ATATGT	CAACTGGA	ATGG	47
qq	 121 Arg		AlaGly					1 14
Qy	480 GACAC	TGA(	GGGGAZ	CGGGGAAAATGGCAC	SCACCGGCCAAAGCCATCA	CCATCATAACGTCTTC	TCCCTGATGGGAAA	A 539
Ωp	141 Asp	- Si	GlyGlu	AsnGlyTh	Glnse	sAsnValP	ProAspGl	s 160
ý d	540 CCT	CTTTTCCT	TCACCACCC	CGGGA	TGGAGAAGATGGAATTT	TTCATCTACGTC	TCTTCCACACACTT	66 6
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දු දු	181 Gly	AGTAT	л— Б—	sAAATTGGG            1LysLeuGl	CAGAAATTGGGACGATGTTCAGTGAGAGTT 	AGTTTCTGTG               gvalServal	TGAACACAGCCAAT 	T 659
<b>%</b>	660 GTGAC	×=	TTGGGCCT	TCAACTCATG	GGAAGTGACTGTCTACAGAAGACATGGA	CAGAAGAC	ATGGACGGGCATAT	r 719
ΟD	201 Val	Thri	31yPro	GlnLe	3luVa	rArgArgH	sGlyArgAlaTy	r 220
<i>ك</i> و و	720 GTTC	CCCATC	GCACAAGTC	GTGAAAGATGTC		ATCAGA	TTCCTGTGTTTGTG	3 779
ò	08	TTC	AGAAC	DOLEGOVE	4 Z			
do do	4	Phe	31nLys	GlnLysAsnAspArgAsn.	Ser!		AAAGAICICCC	26
٥'n	839 ATTA	GTTT	GATGTC	CCTGATTCATG	ATCCTAG	CTCAATT	ATTCTACCATTAAC	868
qa	261 ileN	tPhe	Aspva]	LeulleHi	  spProSe	rHisPheLeuAsnTyrSer		1 280
ζ	T 66	ACAAGTGGAGCTTCG	AGCTTC	GGGGATAA	GGGGATAATACTGGCCTGTTTGT	LTCCAC	CCAATCATACTGTGAA:	T 958
qq	281 Tyri	ystrp	SerPhe	GlyAspAs	nThrGlyLeuPheva	SerThra	- 60	300
δλ	959 CACA(	ACGTATGTGC		TCAATGGAACCTTCAG	CTTCAGCCTTAACCT	CACTGTGA	CCTTAACCTCACTGTGAAAGCTGCAGCACCA	1018
qq	301 His	rhrtyr		AsnGlyrh	rPheSerLeuAsnLe	Thrvall	ysAlaAlaAlaPro	320

WI;

Godowski PJ; ~~ Wood

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The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agoniests and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or anglogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, agerelated macular degeneration, atheroselerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebtis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AlaAlaLySAXGPheHiSASpValLeuGlyAsnGluAxGProSerAlaTyrMetArgGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 GTGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 HisAsnGlnLeuAsnGlyTrpSerSerAspGluAsnAspTrpAsnGluLysLeuTyrPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAAACTCTACCCA
                                                                                                                                                                                                                                                                                                                                                                                                          One hundred and eighty seven nucleic acids encoding PRO polypeptides useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                    Goddard A, Gouche
TF, Watanabe CK,
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Matches:
Conservative:
Mismatches:
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Smith V, Stephan JF,
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Grimaldi JC, Gurney AL,
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N-PSDB; ACA68517.
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Best Local Similarity:
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Claim 11; Fig 42; 315pp; English.
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ACCCTGATITCTGTTCCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCC 1522
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                                               ThrLeuIleSerValProAspArgAspProAlaSerProLeuArgMetAlaAsnSerAla
                                                                                                                                                                                                     LeulleSerValGlyCysLeuAlaIlePheValThrValIleSerLeuLeuValTyrLys
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                                                                                                                                                          CTGATICTCCGTTGGCTTGGCCATATTTGTCACTGTGATCTCCCTTTGGTGTACAAA
                                                                                                                                                                                                                                                                                                                                                                                             LysHisLysGluTyrAsnProlleGluAsnSerProGlyAsnValValArgSerLysGly
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Smith V, Stephan JF, Watanabe CK, Wood
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	Db 341 ThrThrLeuLygSerTyrAspSerAsnThrProGlyProThrGlyAspAsnProLeuGlu 360 Qy 1103 CTGAGTAGGATTCCTGATGAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACC 1162	Db 361 LeuSerArgileFroAspGluAsnCysGlniideAsnArgiyrGlyHisPheGlnAiaThr 380  Qy 1163 ATCCAATTGTAGAGGGAATCTTAGAGGTTAACATCATCGAGAGAGA		1283	1545 IGCAGCCCIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	461	1463 ACCCGATTICTGTTCTGTACAAAACCCAGCCTTTAAGAATGGCAAACAGTCC 1	1523 CTGATCTCCGTTGGCTTGGCCATAITTGTCACTGTGATCTCCCTCTTGGTGTAAA  501 LeulleSerValGlyCysLeuAlailePheValThrValileSerLeuLeuValTyrLys	521	1643 CIGAGIETTICICAACCGIGLAAAACGGIGITICICCGGGAAAACGAAAAAAAAAAAAAAA		Search completed: September 10, 2004, 15:39:40 Job time : 236 secs				
Alignment Scores: Pred. No.: Pred. No.: Sore: Score: Percent Similarity: Pres. Mismatches: Percent Similarity: Pres. Mismatches: Query Match: 61.42% Indels: I	(1-2661) x ABJ72248 (1-572)	120 GCGCCAAACGATTTCATGATGTGCTGGGCAAAGAACCTTCTGCTTACATGAAAGACTTTCATGATGTGCTGGGCAAAGAACGATTTCATGATGCTGGGCAAAGAACGATTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGGG 17	Db   21 AlaAlaLysArgPheHisAspValLeuGlyAsnGluArgProSerAlaTyrMetArgGlu 40	240 GTGTGGAAGCGGGGACATGAGGTGGAAAAACTCCTGGAAGGGAGGCGTGTGCAGGCG 	Qy 300 GTCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTG 359	Qy 360 ATATTCCCTAGATGCCAAAAGGAAGATGCCAACATGGCAACATGGTCTATGAGAAGAACTGC 419	Qy         420 AGAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGGCATGGTCAGAG 479           Db         121 ArgAsnGluAlaGlyLeuSerAlaAspProTyrValTyrAsnTrpThrAlaTrpSerGlu 140	Qy         480 GACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAA 539           Db         141 AspSerAspGlyGluAsnGlyThrGlyGlnSerHi8Hi8A8nValPheProAspGlyLys 160	Qy         540 CCTTTTCCTCACCACCGCGATGGAGAAGTTGGAATTTCATCTACGTCTTCCACACACTT         599           Db         161 ProPheProHisProGlyTrpArgArgTrpAsnPheileTyrValPheHisThrLeu         180	Qy 600 GGTCACTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACACAGCCAAT 659	Oy 660 GTGACACTTGGGCCTCAACTCATGGAAGTGCTCTACAGAAGACATGGACGGCATAT 719	Oy 720 GTTCCCATCGCACAAGATGAAAGATGTGTACGTGACAGATCAGATTCCTGTGTTTGTG 779	OY 780 ACTATGTTCCAGAAGGATGGAAATTCATCGGAGGAACCTTCCC-AAAGATCTCCCC 838	OY 839 ATTATGATGATGATTCATGATCCTAGCACTTCCTCAATTATTCTACCATTAAC 898	Qy 899 TACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTT	QY 959 CACACGTATGTGCTCAATGGAACCTTCAGCTTAACCTCACTGTGAAAGCTGCAGCACCA 1018

us-10-039-272-1.rng

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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

9 September Run on:

2004, 20:21:02; Search time 1483 Seconds (without alignments) 7622.694 Million cell updates/sec

US-10-039-272-1 2661 Title: Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 Gapop 10.0 Scoring table:

3373863 segs, 2124099041 Searched:

6747726 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseg 29Jan04:\* Database :

geneseqn2001as:\*geneseqn2001bs:\* geneseqn2002s:\* geneseqn2003as:\* geneseqn1980s:\* geneseqn1990s:\*geneseqn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqn2003cs:\*
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## ALIGNMENTS

RESULT 1

Human; cell differentiation; white blood cell; bone marrow cell; haematopoietic growth factor inducible neurokin-1; HGFIN; progenitor proliferation; acute myeloid leukemia; non-Hodgkin's disease; acute lymphocytic leukemia; chronic myeloid leukemia; so. chronic lymphocytic leukemia; Hodgkin's disease; gene; ss. Nucleotide sequence of human HGFIN. ABQ78551 standard; DNA; 2661 BP. (first entry) 25-NOV-2002 ABQ78551; ABQ78551
LD ABQ7
XX AC ABQ7
XX XX Huma
XX Huma
XX Huma
XX A AC

Homo sapiens

\_except= (825. .826, aa:Leu) Location/Qualifiers /\*tag= a /product= "HGFIN" /transl\_except= (

WO200262947-A2

15-AUG-2002

20-OCT-2001; 2001WO-US050204.

20-OCT-2000; 2000US-0241881P.

(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

Pranela R;

WPI; 2002-657531/70. P-PSDB; ABB78200 Hematopoietic growth factor inducible neurokin-1 type polypeptide and polynucleotide for treating a disease associated with abnormal bone marrow cell differentiation or proliferation, e.g. leukemia.

Claim 2; Page 121-123; 125pp; English.

The present sequence encodes human haematopoietic growth factor inducible

480 540 540 600 009 099 099 720 720 780 780 neurokin-1 type (HGFIN) polypeptide. HGFIN induces white blood cell differentiation and inhibits progenitor proliferation. HGFIN polypeptides and polymucleotides are useful for treating a disease associated with abnormal bone marrow cell differentiation or proliferation, especially acute myeloid leukemia, acute lymphocytic leukemia, chronic myeloid leukemia, acute lymphocytic leukemia, chronic lymphocytic leukemia, sand non-Hodgkin's 240 240 360 420 480 120 120 180 180 300 300 360 420 09 60 GTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACACAGCCAATG CTTTTCCTCACCACCACGGATGGAGAAGATGGAGAATTTCATCTACGTCTTCCACACACTTG TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGGACGGGCATATG TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAACTCTACCCAG TGTGGAAGCGGGAACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG TGTGGAAGCGGGGAGACACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCA TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCA GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAGG GAAATGAGGCTGGTTATCTGCTGATCCATATGTTTACAACTGGACAGGCATGGTCAGAGG ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCCATCATAACGTCTTCCCTGATGGGAAAC CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTTCATCTACGTCTTCCACACACTTG GTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGGTTTCTGTGAACACAGCCAATG TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA CGGCACGAGGCCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA CCGCCAAACGATTTCATGATGTGTGCCAATGAAAGACCTTCTGCTTACATGAGGGGG ACAATCAATTAAATGGCTGGTCTTCTGATGAAATGACTGGAATGAAAAACTCTACCCAG TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA TGGAATGTCTCTACTATTTCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG rggaargrererarrrecragaarrrergerecragaagarraccattara CCGCCAAACGATTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC CGGCACGAGGCCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA Gaps ., 2661; Other; Indels 0 ë, , 9 . 0 0 .. H DB 100.0%; Score 2661; 100.0%; Pred. No. 0; ive 0; Mismatches G; 716 C; 587 A; 586 Conservative BP; 772 Similarity 2661 Best\_Local Simi Matches 2661; 421 481 481 541 601 601 199 199 721 181 361 421 61 61 121 241 301 301 361 Sequence 121 181 241 Query Match 8 & 8 & 8 경 영 ò Ωp ò q ò g δ g 8 8 8 8 8 엄 상 Db B & B & 0

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Mouse Urogenital Sinus (UGS) tissue was isolated from 17 day old mouse embryos. The UGS cells were infected with retroviruses, cultured and implanted under the renal capsule of mice. Reconstitutions were harvested beeks later, when they showed signs of distress from the tumour burden. RNA was isolated from primary tumours and metastases, reverse transcribed and subjected to differential display PCR. The sequences were analysed to obtain metastatic sequences, e.g. the present sequence. The method can be used to detect, diagnose and treat disorders related to metastasis, or treat malignant or non-malignant disorders, e.g. hyperplasia, dysplasia and hypertrophy. The metastatic sequence can be used to screen a biological sample for metastasis, and it or its expression product may also be used to treat a metastatic disorder
                                                                                                           tumour metastatic sequences - by introducing transfected nost mammal and analysing primary and metastatic sequences
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2669 BP; 752 A; 595 C; 597 G; 725 T; 0 U; 0 Other;
                                                                                                                                                              Disclosure; Fig 12CS; 102pp;
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Length 2669;

2, 17; DB

Score 2547.8; Pred. No. 0; 0; Mismatches

95.7%;

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Indels

119 147 179 207 239 267 299 327 AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACAGCCCCTCG 359 TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG 387 419 447 479 507 539 567 87 599 627 629 AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTCACCAGCCCTCG Accrigasificciccorcordasarricascarasaarcricracrarriccressar TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGGAGACATGAGGTGGA TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG CCAATGGCAACATAGTCTATGAGAAGTACTGCAGAAATGAGGCTGGTTTATCTGCTGATC CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAATGAGGCTGGTTTATCTGCTGATC CATATGTTTACAACTGGACAGGATGGTCAGAGGACAGTGACGGGGAAAAATGGCACCGGCC AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA GATGGAATITCALCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT 268 300 328 360 388 420 448 208 268 ò Db Dp  $\dot{\delta}$ à g ò ρp ð g g ð

cancer; metastatic sequence; detection; diagnosis; hyperplasia; dysplasia; hypertrophy; screening;

metastatic nucleic acid sequence.

tumour;

treatment; metastasis; murine;

musculus WO9718454-A2

Mus

22-MAY-1997

(first entry)

26-FEB-1998

Murine

95US-0006838P 96US-00594031 96WO-US018567

16-NOV-1995; 30-JAN-1996; 15-NOV-1996;

2669

AAT69328 standard; cDNA;

1740 TACTOMARACORGANITION OF CONTROLL AND THE CONTROLL TO TACTOMARACORGANICAL TO TACTOMARACORGANICAC TO TACTOMARAC	JT 3 AAT69318 standard; CDNA; 2669 BP. AAT69318; 26-FEB-1998 (first entry) Murine metastatic nucleic acid sequence.
8	RESULT 3 AAT6931E ID AAT XX AC AAT XX AC AAT XX DT 26- XX XX DB MUI
6.8 GITCAGTORAGACTITCTOTANACAGACCAATTTACTOGACCTCAACTCAATCATGAAGA 6.8 TACATCACACAACTTTCTOTAACACACACAATTTACTCCAACTCAACACAAATTTACTTTACTTACACACACACAATTTACTCCAACTCAACAA	1587 ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGCCTGA 1646

Ω.

diagnosis;

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Mouse; murine; tumour; cancer; metastatic sequence; detection; diagnos treatment; metastasis; hyperplasia; dysplasia; hypertrophy; screening;
                                                                                               WPI; 1997-289397/26
                                                                            (THOM/) THOMPSON T.
                                 WO9718454-A2
                        musculus
                                                    LS-NOV-1996;
                                                                   30-JAN-1996;
                                                             16-NOV-1995
                                           22-MAY-1997
                                                                                      Thompson T;
                        Mus
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95US-0006838P. 96US-00594031. 96WO-US018567

Mouse Urogenital Sinus (UGS) tissue was isolated from 17 day old mouse embryos. The UGS cells were infected with retroviruses, cultured and implanted under the renal capsule of mice. Reconstitutions were harvested beeks later, when they showed signs of distress from the tumour burden. RNA was isolated from primary tumours and metastases, reverse transcribed and subjected to differential display PCR. The sequences were analysed to obtain metastatic sequences, e.g. the present sequence. The method can be treat malignant or non-malignant disorders, e.g. hyperplasia, dysplasia and hypertrophy. The metastatic sequence can be used to screen a biological sample for metastasis, and it or its expression product may also be used to treat a metastatic disorder. Identifying tumour metastatic sequences - by introducing transfected cells into host mammal and analysing primary and metastatic sequences differential display PCR. Disclosure, Fig 12BT; 102pp; English.

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Sequence 2669 BP; 752 A; 595 C; 597 G; 725 T; 0 U; 0 Other;

a ò g

119 147 179 207 ATGAAAATGACTGGAATGAAAACTCTACCCAGTGGAAAGCGGGGAAAACATGAGGTGGA 267 327 359 TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCAAAAGGAAGAAG CCAAIGGCAACAIAGICIAIGAGAAGAACIGCAGAAAIGAGGCIGGIITAICIGCIGAIC 447 Accricaerdccrcccrcacaarrcacardcardcarcrcrcracrartrcrcrcacar TTCTGCTCCTGGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG Tricidenteriological de la contra dela contra de la contra de la contra de la contra de la contra dela contra de la contra del la contra de la contra del AACCITGGTGCCTGCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCACTCG ATGAAAATGACTGGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGGAGACATGAGGTGGA AAAACTCCTGGAAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGAAGATG Gaps 3; Length 2669; Indels 95.7%; Score 2547.8; DB 2; 99.2%; Pred. No. 0; ive 0; Mismatches 17; Conservative Similarity Best Local Sim Matches 2591; 28 09 Match 88 120 148 180 208 240 268 300 328 360 388

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1019 CCATIGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC 479 1106 1139 1166 1199 567 1226 1259 1286 1346 627 629 719 1406 1439 1466 1499 687 747 779 1319 1526 807 839 866 899 926 959 986 CATATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAAATGGCACCGGCC AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT GTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG GTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG TGACTGTCTACAGAAGACATGGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT CATCCGACGAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG GCCTGTTTGTTTCCACCAATCATGTGAATCACACGTATGTGCTCAATGGAACCTTCA GCCTGTTTGTTTCCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCACCAC 1020 GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCGCCACGCCACCACCAC CCAGACCTTCAAAACCCACCCCTTCTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGA GTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA CAGACCTTCAAAACCCACCCTTCTTTAGGACCTGCTGGTGGAACCCCTGGAGCTGA GTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA CAATTGTAGAGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGG TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCA TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCA CGGAGGICIGIACCATCATITCIGACCCCACCIGGAGAICACCGAGAACACAGAGICIGCA GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG GGACGTACTGTGTGAACCTCACCCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC TGATTICTGTTCCTGACAGACCCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA 480 540 420 448 508 568 009 628 099 688 720 748 780 808 840 960 867 006 927 987 1047 1080 1140 1107 1167 1200 1227 1260 1287 1320 1347 1440 1467 1380 1407 à 셤  $\delta$ g ò qq DP à à 임 ò g δ Бb  $\delta$ g à qq dd à à g d ò à 셤 ð qq ò g ð g ò g ð

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The present invention describes a method for screening drug candidates.

The method comprises adding a drug to a cell that expresses an expression profile gene encoding a protein encoded by 5 sequences of defined base profile gene encoding a protein encoded by 5 sequences of defined base comparison in C55619, C55614, C55614, C55614 and C55630 or a sequence comparison of the expression number X9251, X6246, J04130, X62087 and X76534 (or a fragment) and determining the effect of the drug on the expression profile gene. An inhibitor of matrix metalloproteinase 19 (MMD-19), preferably an antibody, is useful for treating destructive macrophage disorders (DMD) by inhibiting DM development in a cell of an individual having arthritis. Antibodies to MMD-19 are useful for localising a therapeutic moiety preferably cyclocaric agent or a radioisotope to colorectal cancer tissue. A composition comprising MMP-19 is useful for eliciting an immune response in an individual. C55635 to C55710 represent human differentially credible comparison of the invention. The present sequence represents the human NMB cDMA sequence according to the Genbank accession number X76534.

It is specifically claimed by its Genbank accession number is not in the present specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening drug candidates comprises adding a drug to a cell expressing an expression profile gene and determining the effect of the drug on the expression of the expression profile gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; differentially regulated gene; macrophage development; diagnosis;
matrix metalloproteinase 19; MMP19; antiarthritic; antiinflammatory;
destructive macrophage development inhibitor; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acciricagiecciecerecereagaarreagearegaarerereracrarriceregaar
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NMB cDNA sequence from Genbank X76534.
                                                         2639 TAAAGTGTGGGAAGAGACAAAAAAAAAAA
2607 -AAAATGAGGGAAGAGACAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colorectal cancer; immune response; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2000; 2000WO-US006883
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Matches 2591; Conserv
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120 TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG 179  148 GCAATGAAAGACTTCTGCTTACATGAGGGAGCACAATCAAT		CCANTGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTC CATATGTTTACAACTGGACAGCATGGTCAGAGGCACAGGGAAAATGGCA [	5.90 AAAGCCAICAICAICAICAIGGGAAACCTITICCTCACCACCCGGAIGGGAAA 599 568 GAIGGAAITTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCACAAATTGGGACGAT 627 600 GAIGGAAITTCATCTACGTCTTCCACACATTGGTCAGTATTTCCAGAAATTGGGACGAT 659 628 GITGGAAITTCTGTCAACACACATGTGAACACTTGGTCAGAAATTGGGACGAT 659	660 GTTCAGTGAGAGTTTCTGTGAACACAGCCATGTGACACTTGGGCCTCAACTCATGGAAG 719 688 TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAGAGAAAGATGT 747 720 TGACTGTCTACAGAAGACATGGACGGCATATGTTCCCATCGCACAGAGAAGATGTT 779		TACTG	960 GCCTTAACCTGACAATGCTGCAAATCACGGAACCTTCA 986 960 GCCTGTTTGCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA 1019 987 GCCTTAACCTGACTGGAAAGCTGCAGGACCTTGTCGCCACCGCCACCACCACCACTTCATGTGAATGGAACCTTCATGTCACCACCACCACCACCACCACCACCACCACCACCACCAC			1167 CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGG 1226

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CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG 926
              involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome or fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated cDNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCAGTGAGAGTTTCTGTGAGACACAGCGAATGTGACACTTGGGCCTCAACTCATGGAAG
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induced abnormalities in bone formation or bone loss, conditions that
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                                                                                                                                                                                                                   Length 2669;
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99.2%; Pred. No. 0;
cive 0; Mismatches
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Best Local Similarity 99.2
Matches 2591; Conservative
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                                                                                                                                                                                                                                                                                                                                                   AAAAATTTGGTCCCTGGTTTTTCATGGCAACTTGATCAGTAAGGATTTCCCCCTCTGTTTG
                                                                                                                                                                                                                                                                                                          2519 AAAGAHGAGGICCCTGGITITICAIGGCAACTIGAICAGIAAGGAITICACCICIGIIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; osteoblast; stem cell differentiation; bone tissue deposition;
                                                                                                                                                                                                                                2460 TATTTCCAAATTTTTGTATAGTCGCTGCACATATTTGAAATC-ATATATTAAGACTTTCC
                                GTGACAACCTACTTTGCTTGGCTGAGGGAATGATATTCATATTCATTTATTCCA
                                                             2400 resacarriastrasiscririrararaccasscarsarscreasracacricristara
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L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2000; 2000US-0255882P.
24-APR-2001; 2001US-0285691P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .8-DEC-2001; 2001WO-US048276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENE LOGIC INC.
(PROC ) PROCIER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Mertz
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719 747 779 807 839 866 899

629 687

567 599 627

539

479 507

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Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
                                                                                                                                       Claim 22; Page 327-328; 453pp; English
                                   EOS BIOTECHNOLOGY INC.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-0372246P.
                                                                                                                        expression in lung cancer
                                                                    WPI; 2003-093161/08
P-PSDB; ABU56592.
                                                   Murray R;
                                                                                                                                                                                                                                                                                                               invention
                                   (EOSB-)
                                                   Aziz N,
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer compound that modulates a lung cancer-associated polypeptide for identifying a compound that modulates a lung cancer-associated polypeptide. For inhibiting proliferation of a lung cancer-associated polypeptide. For cinhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by cancering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell ung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, thypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis, bronchiectasis. The genes, polymucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences and as targets for screening for therapeutic approximately approximate that modulate that encare, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of

479 119 147 299 327 387 447 179 207 267 448 CATATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAATGGCACCGGCC 507 87 TGGGCTCAAATATAAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG TTCTGCTCCTGCTGCAGATGCCCACTTGATGCCGCCAAACGATTTCATGATGCTGC AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG resecricaaararaacarringcesreaaccreararricecraeareccaaaagaasa CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC AACCTTGGTGCCTGCGTCCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT ACCTTGAGTGCCTGCGTCCGTGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG **ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGAGACATGAGGTGGA** AAAACTCCTGGAAGGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG Gaps ٠, ش Length 2669; Sequence 2669 BP; 752 A; 595 C; 597 G; 725 T; 0 U; 0 Other; Indels DB 7; 17; Score 2547.8; Pred. No. 0; 0; Mismatches 95.78; Query Match
Best Local Similarity 99.2
Matches 2591; Conservative 28 9 88 148 180 208 240 268 300 328 360 388

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                                                  GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGGAAAACCAGGAAAAGGATCCGC
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Neuroprotective; Nootropic, Antianemic; Antiarteriosclerotic; Antiinflammatory; Opthalmological; Muscular; Hepatotropic; Neuroprotective; Antiasthmatic; Anticonvulsant; Virucide; Antibacterial; Fungicide; Antiparastic; Protozoacide; Antihelminthic; Cytostatic; Cerebroprotective; Antiparkinsonian; Antipsoriatic; Antigout; Antidout; Antihelminthic; Osteopathic; Gene therapy; Antidatabetic; Antirheumatic; Osteopathic; Gene therapy; human; cell growth; cell differentiation; cell death; CGDD; cell proliferative disorder; cancer; developmental disorder; neurological disorder; autoimmune disorder; inflammatory disorder; infection; reproductive disorder; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kable AE, Tran UK, Hafalia AJA, Burford N, Honchell CD, Lehr-Mason PM, Duggan BM, Ramkunar J, Griffin JA, Richardson TW Elliott VS, Jiang X, Jackson AA, Marquis JP, Chawla NK, Khare Becha SD, Lee SY, Swarnakar A, Yue H, Warren BA, Baughn MR, L
                                                                                                                           Anabolic; Hypertensive; Respiratory; Anti-HIV; Antiallergic;
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                                                                                                Human CGDD-16 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2002; 2002US-0364494P.
29-MAR-2002; 2002US-0369129P.
12-APR-2002; 2002US-0372511P.
                        ADD78274 standard; DNA; 2728
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                                                                          (first entry)
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Gandhi AR,
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Becha SD, Lee SY
Lee S, Ho A, Ga
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Ho A,
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                                                                        29-JAN-2004
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RESULT 7
ADD78274
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\*W polypeptides and polynucleotides associated with cell growth, fferentiation and death, useful for diagnosing, treating or preventing g. developmental, neurological, autoimmune, inflammatory or reproductive disorders e.g.

2003-779081/73.

WPI; 2003-779081/ P-PSDB; ADD78235.

PG;

SEQ ID NO 55; 320pp; English. Claim 5;

The present invention relates to novel human proteins (1; ADD78220-ADD78288) and their coding sequences (II; ADD78259-ADD78297), which are associated with cell growth, differentiation and death, referred to as CGDD-n proteins, where n is a number from 1 to 39. The CGDD proteins and their coding sequences are useful for diagnosing, treating or preventing cell proliferative disorders (e.g. cirrhosis, hepatitis, arteriosclerosis, poriasis, primary thrombocytopenia) or cancers (e.g. arteriosclerosis, poriasis, primary thrombocytopenia) or cancers (e.g. denocarcinoma, sarcoma or cancers of the bone, bone marrow, brain, breast, colon, kidney, liver, lung or uterus), developmental disorders (e.g. tenal tubular acidosis, Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism or selzures), neurological disorders (e.g. Pick's disease, cataract, epilepsy, ischemic cerebrovascular disease, stroke, Alzheimer's disease, Parkinson's disease or dementia), autoimmune/inflammatory disorders (e.g. AIDS, allergies, anemia, asthma, diabetes mellitus, bronchitis, orteoporosis, osteoarthritis, rheumatoid arthritis, contact dermatitis or gout), viral, bacterial, fungal, contact dermatitis or gout), viral, bacterial, fungal, contact dispersion or helminthic infections, reproductive disorders (e.g. riferial), e.g. riferialis, contact dermatitis infections, reproductive disorders (e.g. riferialis). (e.g. infertility, ectopic pregnancy, premature ovarian failure, delayed puberty or prostatitis) or disorders of the placenta (e.g. preeclampsia,

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choriocarcinoma, placenta previa, placental or maternal floor infarction or chronic villitis).  Sequence 2728 BP; 778 A; 610 C; 607 G; 733 T; 0 U; 0 Other;  Query Match  Best Local Similarity 97.8%; Pred. No. 0;  Matches 2596; Conservative 0; Mismatches 19; Indels 39; Gaps 4;	28 AACCTIGGIGCCIGCGIGGGAALTCAGCAIGGAAIGICICIACIAITICCIGGGAI 87	88 ITCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAAGGATTTCATGATGTGCTGG 147 	148 GCAATGAAAGACCTTCTGCTTACATGAGGGAGCACAAATCAATTAAATGGCTGGTCTTCTG 207 	208 ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGGAGACATGAGGTGGA 267 	268 AAAACTCCTGGAAGGGAGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG 327 316 AAAACTCCTGGAAGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG 375	328 IGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG 387 	388 CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC 447 	448 CATATGTTTACAACTGGACAGGACGGGGGACAGTGACGGGGAAAATGGCACCGGCC 507 	508 AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCGGATGGAGAA 567	568 GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT 627 616 GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT 675	628 GTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG 687 676 GTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG 735	688 TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAGTGAAAAAGATGTGT 747 	748 ACGIGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT 807 	808 CATCCGACAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC 866	867 CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG 926	927 GCCTGTTTGTTTCCACCAATCATACTGTGAATCACGTATGTGCTCAATGGAACCTTCA 986
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Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; ss.
                                                                 encoding human PRO protein, Seq ID No 41.
                                                                                                                                                                                       29-JUN-2001; 2001WO-US021066
                                              (first entry)
          ABK33556 standard; cDNA;
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                             ABK33556;
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AACCTTGGTGCCTGCGTCCGTGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT

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TTCTGCTCCTGGCAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG

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ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGGAGACATGAGGTGGA ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAAGCGGGGAAGACATGAAGTGGA

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20-JUL-2000, 2000US-0219556P. 25-JUL-2000, 2000US-0220585P. 25-JUL-2000, 2000US-0220605P. 25-JUL-2000; 2000US-0220607P. 25-JUL-2000, 2000US-0220634P. 25-JUL-2000, 2000US-0220634P.

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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for the proliferation of cancer, and inhibiting the proliferation of normal human blood, for stimulating or inhibiting the proliferation of normal human dermal flor bushast cells. The PRO polypeptide may also be used as molecular wighth markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABR3356. Tepressent human PRO protein coding sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.
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Smith V, Stephan JF,
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; Mismatches
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2000US-0220664P.
2000US-022066F.
2000US-022083P.
2000US-022133P.
2000US-022133P.
2000WO-US023128.
2000WO-US023328.
2000WO-US023328.
2000WO-US03328.
2000WO-US03328.
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Gurney AL,
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Matches 2576; Conserv
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                                                            01-AUG-2000;
22-AUG-2000;
23-AUG-2000;
                                                                                                          24-AUG-2000;
10-NOV-2000;
28-NOV-2000;
01-DEC-2000;
                25-JUL-2000;
26-JUL-2000;
28-JUL-2000;
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20-DEC-2000;
28-FEB-2001;
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Pred. No. 0;

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Conservative

2576;

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97.88;

Similarity

Local

109 147 169

ACCTTGAGTGCCTGCGTCCGTGAGAATTCAGCATGGAATGTCTCTATATTCCTGGGAT TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG trcrecricerecracaadarreceacuraareceacaaacaarrecaraarerec ATGAAAATGACTGGAAATGAAAAACTCTACCCAGTGTGGAAGCGGGGGAGACATGAGGTGGA

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148 170 208

AACCTTGGTGCCTGCGTCCGTGAAATTCAGCATGGAATGTCTCTACTATTCCTGGGAT

207

229 267 289 327 349 387 409 447

TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG 

350 388 410

328

CCAATGGCAACATAGTCTATGAGAAGTGCAGAAATGAGGCTGGTTTATCTGCTGATC

AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski PJ;
`` ^K. Wood WI;
TGGCAACTTGATCAGTAAGGATTTCCCCTCTGTTTGGAACTAAAACCATTTACTATATGT
                                                               CTGCACATATTTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCA
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                                                                                                                                                                                                                                 TAGACAAGACATTTTTTTTTTTCCTTGAAAAA-AAAATGAGGGAAGAACA
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Smith V, Stephan JF,
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; 2001WO-US017800.
; 2001WO-US021066.
; 2002US-00119480.
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CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC
                                                                                                                 AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCGGGATGGAGAA
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                                                          CGTATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAATGGCACGGGCC
                                                                                                AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCGGATGGAGAA
                                                                                                                                                         GATGGAATTTCATCTACGTCTTCCACACTTGGTCAGTATTTCCAGAAATTGGGACGAT
                                                                                                                                                                                 GATGGAATTTCATCTACGTCTTCCACACTTGGTCAGTATTTCCAGAAATTGGGACGAT
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Length 2683;

DB 7;

Score 2485;

93.4%;

Query Match

Sequence 2683 BP; 751 A; 604 C; 596 G; 732 T; 0 U; 0 Other;

useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or wounds in a mammal.

Claim 2; Fig 41; 314pp; English

The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, blosensors or bioreactors. These are tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour. Or a mammal, for atimulating the release of TNF-alpha from human blood, cells, for stimulating proliferation of deficentiation of chondrocyte cells, for stimulating proliferation of pericyte cells, or for modulating normal human dermal fibroblast proliferation. The PRO nucleic acid or polypeptide is also useful for treating tumours or various bone and/or carillage disorders (e.g. sports injuries or arthritis), or wounds. The catilage disorders (e.g. sports injuries or atthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therepeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

Sequence 2683 BP; 751 A; 604 C; 596 G; 732 T; 0 U; 0 Other;

39; DB 7; Length 2683; 20; Indels Score 2485; DB Pred. No. 0; 0; Mismatches 97.88; 93.48; Query Match
Best Local Similarity 97.8
Matches 2576; Conservative

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Qy Up	568	568 GATGGAATTTCATCTACGTCTTCCACACTTGGTCAGTATTTCCAGAAATTGGGACGAT 627 
\$ <del>2</del> 8	628	GITCAGIGAGATITCIGIGAACACAGCCAAIGIGACACTIGGGCCTCAACTCAIGGAAG 687 
P	688	TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAAAGTTT 747 
δλ	748	ACGIGGIAACAGAITCCIGIGITTGIGACIAIGITCCAGAAGAACGAICGAAAIT 807
Db	770	ACGIGGIAACAGAICAGAITCCIGIGIIIIIIIIIIIIII
\(\delta \)	808	CATCCGACGAAACCITCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC 866
δγ	867	CTAGCCACTTCCTCATTATTCTACCATTAACTACAGTGGAGCTTCGGGGATAATACTG 926
QQ Q	890	CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATAATACTG 949
ζ,	927	GCCTGTTTGTTTCCACCAATCATACTGTGAATCACGCTATGTGCTCAATGGAACCTTCA 986
QD	950	GCCIGITIGITICCACCAATCATACTGIGAATCACACGTATGIGCTCAATGGAACCTTCA 1009
හි සි	987	GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCA
<u>a</u>	1010	GULTIAAULIUAUIGIGAAAGCIGCAGCACCAGGACCTIGICCGCCACCGCCACCACCAC 1069
දු දු	1047	CCAGACCTTCAAAACCCACCCTTCTTT
٥y	1075	AGGACCTGCTGCTGACAACCCCCTGGAGGTAGGATTCCTGATGAAAACTGCC 1130
QC	1130	CCCCAGGACCTACTGGTGACACACCCCTGGAGCTGAGGATTCCTGATGAAAACTGCC 1189
ò	1131	AGATTAACAGATATGGCCACCACCACCATCACAATTGTAGAGGAATCTTAGAGG 1190
Db	1190	AGAITAACAGATAIGGCCACTIICAAGCCACCATCACAATIGTAGAGGGAAICTIAGAGG 1249
δγ	1191	TIAACAICAICCAGAIGACAGACGICCIGAIGCCGGIGCCAIGGCCIGAAAGCICCCIAA 1250
QQ	1250	TTAACATCCAGAIGACAGACGICCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAA 1309
δλ	1251	TAGACITIGICGIGACCIGCCAAGGGAGTCCCACGGAGGTCIGIACCATGATITCIG 1310
Db	1310	TAGACTITGICGIGACCIGCCAAGGGAGCAIICCCACGGAGGICTGIACCAICATTICIG 1369
οχ	1311	ACCCCACCTGCGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGGATGTGGATGTT 1370
Db	1370	ACCCACCTGCGAGATCACCCAGAACACACTCTGCAGCCCTGTGGATGTGGATGAGATGT 1429
δy	1371	GTCTGCTGACTGTGAGGACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACC 1430
QQ	1430	GTCTGCTGACTGTGAGAGGAACCTTCAATGGGTCTGGGACGTACTGTGTGAGACCTCACCC 1489
٥'n	1431	TGGGGATGACACAAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAGGACC 1490
Ob	1490	TGGGGGATGACACAGGCTCTCACGAGCACCCTGATTCTGTTCCTGACAGAGACC 1549
δý	1491	CAGCCTCGCCTTTAAAGGATGGCAAAACAGTGCCCTGATCTCCGTTGGCTTGGCCATAT 1550
QQ	1550 (	CAGCCICGCCITTAAGGAIGGCAAACAGIGCCCIGAICICGGIIGGCIGCTIGGCAAAT 1609
ζō	1551	TIGICACTGIGATCTCCCTTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAA 1610
DÞ	1610	TIGICACTGIGATCICCCICITGGIGIACAAAAACACAAGGAATACAACCAACCCAATAGAAA 1669

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Query Match
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The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, agerelated macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation bushers, and in chromosome and gene mapping. This sequence encodes a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
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shan JF, Watanabe CK,
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97.8%;
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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P-PSDB; ABU82068.
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Matches 2576; Conserv
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25-JUN-2003
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ACA68517 standard; cDNA; 2683

RESULT 11 ACA68517 ID ACA6 XX us-10-039-272-1.rng

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CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATAATTGTG
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Sequence 2683 BP; 751 A; 604 C; 596 G; 732 T; 0 U; 0 Other;
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                                                                                     0; Mismatches
                                          Score 2485;
Pred. No. 0;
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illarity 97.8%;
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Matches 2576; Conserv
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                                                                                                                                                                                                                                                                   2569 TGGCAACTTGATCAGTAAGGATTTCACCTCTGTTTGTAACTAAAACCATCTACTATGT
  TGGCAACTTGATCAGTAAGGATTTCCCCTCTGTTTGGAACTAAAACCATTTACTATATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; ss; differentiation; dermal fibroblast; tumour; gene therapy; gene;
                                                                                                              2450 TATACCAGGCATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTTGTACAGTCG
                                                                                                                                                       CTGCACATATTTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCA
                                                                                                                                                                                                                                                                                                                                TAGACAAGACATTTTTTTTTTTCCTTCCTGAAAA-AAAATGAGGGAAGAGACA 2624
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Smith V, Stephan JF, Watanabe CK, Wood
                                                                     TATACCAGGCATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTT
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GCCTTAACCTCACTGTGAAAGCTGCACCAGGACCTTGTCCGCCACGGCCACCGCCACCGC GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGAACCTTGTCCGCCACCGCCACCGCCACCACCACCAC

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GCCTGTTTGTTTCCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA

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The invention relates to a novel isolated PRO protein encoding nucleic acid. The nucleic acid of the invention may be useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a tumour in a mammal. Furthermore, the molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells, the release of tumour necrosis factor (TNF)-alpha from human blood, the proliferation or differentiation of chondrocyte cells and for inhibiting the proliferation of normal human dermal fibroblast cells. Finally, the molecules may be utilised during gene therapy. The current sequence is that of the human PRO cDNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGIGGIAACAGAITCCTGIGITTGIAGACIATGITCCAGAAGAACGAICGAAATT
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ME, Goddard A, Godowski PJ; Stephan JF, Watanabe CK, Wood WI;

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New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes.
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2001WO-US021066.
2002US-00119480.
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The invention relates to an isolated mucleic acid encoding a PRO polypeptide. Nucleic acids that encode PRO can be used to generate either transgenic animals or knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy for replacing defective gene, in chromosome identification, as chromosome markers, or in generating probes to isolate full length PRO CDNA. The PRO polypeptides are useful for chondrocyte stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation and the isolated nucleic acids may be used for recombinantly expressing and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for pro and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents cDNA encoding a human expression expression that all sequence represents cDNA encoding a human
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28-AUG-2002; 2002US-00230338

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us-10-039-272-1.rng

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This invention relates to one hundred and twenty two novel nucleic acids encoding human PRO membrane bound proteins or receptors. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically coverned by information received from other cells and the immediate of polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as proteins. These membrane bound proteins and proteins and proteins of the coptors and diagnostic agents, such as in the blocking of receptor content interpreted by diverse cell receptors and proteins along with the cDNA sequences encoding them. The novel proteins of the convention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a membrane bound respect to the copy of a tumour associated gene. The present sequence is the cDNA may have copy the copy of the measuring or detecting the copy may not account of the measuring or detecting the copy may not not they may be useful for measuring or detecting the copy manual. In addition, they may be useful for measuring or detecting the copy manual.
                                                                                                                                                                                          Human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour; gene; ss.
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Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                         Human membrane bound receptor/protein PR09925 cDNA sequence.
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24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
01-UIN-2001; 2010WO-US021066.
29-JUN-2002; 2002US-00119480.
                                       ABT43902 standard; cDNA; 2683
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RESULT 15
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Gaps

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20; Indels

93.4%; Score 2485; DB 8; Length 2683; 97.8%; Pred. No. 0; ive 0; Mismatches 20; Indels 39

Query Match
Best Local Similarity 97.8
Matches 2576; Conservative

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	Qy 1191 Db 1250 Qy 1251 Db 1310			Oy 1551 Db 1610 Oy 1611			Oy 1917 Db 1977 Oy 1977 Db 203	Oy 209 Oy 209 Db 215 Oy 215

2269 2270 2329 2330 2389 2390 2449 2450 2509 2510 2568 2570 2628 2210 GITICTAAGAICAIGIICCAAGCIAACTGAAICCCACTICAAIACACACTCATGAACTCC 2391 TATACCAGGCATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTTGTATAGTCG 2450 TATACCAGGCATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTTGTACAGTCG CIGCACATATITGAAATC-ATATAAAGACTITCCAAAGATGAGGTCCCTGGTTTTTCA 2569 IGGGAACTIGATCAGTAAGGATTIGACTCTGTTIGTAACTAAAACCATCTACTATATGT 2270 TGATGGAACAATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGAACTCAGAA 2451 CIGCACATATITGAAATCAAAATATTAAGACTITCCAAAAATTTGGTCCCTGGTTTTTCA 2511 TGGCAACTTGATCAGTAAGGATTTCCCCCTCTGTTTGGAACTAAAACCATTTACTATATGT 2629 TAGACATGACATTCTTTTTCTCTCTGAAAAATAAAGTGTGGGAAGAGACA 2683 TGATGGAACAATAACAGGCCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAA TAGACAAGACATTTTTTTTTTTCCTTGAAAA-AAAATGAGGAAGAACA 2624 2510 2571 2211 2331 qq qq qq  $\delta$ S P ò a δ à  $\delta$ ò du

Search completed: September 10, 2004, 02:34:51 Job time: 1498 secs

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Sequence 225, App
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McNeill, Patricia D.
Fanger, Neil
WENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
US-09-735-705-225
US-09-880-716A-225
US-09-980-716A-225
US-09-943-075A-6
US-09-943-075A-6
US-10-007-700-225
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US-10-232-224-42
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US-10-219-076-42
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US-10-219-474-42
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CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
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Patent No. US20020052329A1
GENERAL INFORMATION:
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
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Li, Samuel X.
Wang, Aijun
Skeiky, Yasir A.W.
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-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model - NATRIX=blosum62
-LOOPCL=0 -LOOPCRI=0 -UNITS=blts -GTART=1 -END=-1 -MATRIX=blosum62
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-THR MINE 0 -ALIGN=L5 -MODE=LOCAL -OUTFMT-pto -NORM=xt -HRAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USR=US10039272 GGGN 1 1.262 @runat n7092004 144225.21764
-NCPU=6 -ICPU=3 -NO MMAP -LARGSQUERY -NEG SCORES=0 -WAIT -DSPBLOGR=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                           September 10, 2004, 15:48:34; Search time 569.5 Seconds (without alignments) 2996.857 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                - protein search, using frame_plus_n2p model
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Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1335176 seqs, 320689617 residues

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1199 ATCCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTT
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                               CACACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCA
                                          CCTGCTGGTGACAACCCCCTGGAGCTGAGGATTCCTGATGAAAACTGCCAGATTAAC
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Sequence 225, Application US/09850716A

Patent No. US2002011519A1

GENERAL INPORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND INSTHODS FOR THE THERAPY
TITLE OF INVENTION: US/09/850.716A

FILE REFERRINCE: 210121.455015
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440

SEQ ID NO 225

LENGHARE: FastSEQ for Windows Version 3.0

LENGHARE: FastSEQ for Windows Version 3.0
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Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
       ; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: HOMO S
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Fatent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Mangerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: CAMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
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Sequence 6, Application US/09943075A

Sequence 6, Application US/09943075A

Sequence 6, Application US/09943075A

Sequence 6, Application US20020151486A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Safedo, Fayez F.
APPLICANT: Safedo, Fayez F.
APPLICANT: Safeov, Exeven N.
TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same,
TITLE OF INVENTION: Osteoactivin Protein and Methods of Stimulating Bone Differentiation
FILE REFERENCE: 71369,262

CURRENT APPLICATION NUMBER: US/09/943,075A

CURRENT APPLICATION NUMBER: US 60/229,006

PRIOR FILING DATE: 2001-08-30

PRIOR FILING DATE: 2000-08-30

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Li, Samual X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: Panger, Noil
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Retter, Marc W.
Durham, Margarita
Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
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      APPLICANT: Watanabe, Yoshihiro
APPLICANT: Peckman, David W.
APPLICANT: Peckman, David W.
APPLICANT: Cai, Fend
APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: PastSEQ for Windows Version 4.0
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Mismatches:
Indels:
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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US-10-007-700-225
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FILE REFERENCE: 267/033 University of Medicine & D CURRENT APPLICATION NUMBER: US/10/463,106
CURRENT FILING DATE: 2003-06-17
PRIOR APPLICATION NUMBER: US 10/039,272
PRIOR FILING DATE: 2001-10-20
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTING PATE: 2000-10-20
SOFTWARE: PATENTING DATE: 2000-10-20
SOFTWARE: PATENTING DATE: 2000-10-20
SOFTWARE: PATENTING DATE: 2000-10-20
SOFTWARE: PATENTING DATE: 2000-10-20
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                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20020168653A1
GENERAL INFORMATION:
APPLICANT: RAMESHWR,
TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-TYPE
FILE REFERENCE: 267/033 University of Medicine & Dentistry of New Jersey
CURRENT APPLICATION NUMBER: US/10/039,272
                                                                                           ThrMetPheGlnLysAsnAspArgAsnSerSerAspGluThrPheLeuLysAspLeuPro
                                                                    ATTATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAAC
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                                                   ATCCAGATGACGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTT
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             NS-10-117-982-225

Sequence 225, Application US/10117982

Publication No. US20030138438A1

Publicantion No. US20030138438A1

APPLICANT: Foy, Teresa M.

APPLICANT: Foyer Cary R.

APPLICANT: Carier, Darrick

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Watenabe, Yoshihiro

APPLICANT: Watenabe, Michael D.

APPLICANT: Malos, Michael D.

APPLICANT: Maricle, Barbara
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   ; CURRENT FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/241,881
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-272-2
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                  ACTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCC-AAAGATCTCCCC
                            ThrMetPheGlnLysAsnAspArgAsnSerSerAspGluThrPheLeuLysAspLeuPro
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Publication No. US20030232350Al
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
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                               ND METHODS FOR OF LUNG CANCER
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APPLICANT: Spies, Gregory A.
APPLICANT: Fan, Liqun
APPLICANT: Mang, Trongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG C,
FILE REPERENCE: 210121.455C18
CURRENT APPLICATION NUMBER: US/10/117,982
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 484
SOFTWARE: FastSRQ for Windows Version 4.0
SEQ ID NO 225
LENGTH: 560
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    APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Matron, Susan R.
APPLICANT: Watron, Susan R.
APPLICANT: Watron, Susan R.
APPLICANT: Watron, Susan R.
APPLICANT: Watron, Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer TITLE OF INVENTION: Methods of Screening for Modulators of Cancer TITLE OF INVENTION: Methods of Screening for Modulators of Cancer PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR PLING DATE: 2001-11-15
PRIOR PLING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PLING DATE: 2001-11-21
PRIOR PLING DATE: 2002-01-08
PRIOR PLING DATE: 2002-01-08
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TYPE: PRT
ORGANISM: Homo sapiens
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OY 1499 CCTTPAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTGCCCATATTTGTCACT	225 No. US2030236209A1 No. US2030236209A1 No. US2030236209A1 Foy, Teresa M. McManabe, Andria Matanabe, Voshihiro Reed, Steven G. WRANTION: COMPOSITIONS AND METHODS FOR THE THERAPY VENTION: COMPOSITIONS AND LAGARER VENTION: AND DIAGNOSIS OF LUNG CANCER NCE: 2.10121.455C19 LING DATE: 2.002-12-04 EQ ID NOS: 560 astSEQ for Windows Version 4.0  Homo sapiens  Homo sapiens	Alignment Scores:

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NUMBER OF SEQ ID NOS: 274
SOFFWARE: CuraSeqList version 0.1
SEQ ID NO 152
LENGTH: 560
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ORGANISM: Homo sapiens
US-10-309-290-152
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US-10-309-290-152
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CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 466
LENGTH: 560
TYPE: PRT
ORGANISM: Homo sapiens
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| Publication No. US20040101874A1
| GENERAL INFORMATION:
| APPLICANT: Ghosh, Soin D. D. APPLICANT: Fahy, Boin D. APPLICANT: Taylor, Bradford W. APPLICANT: Glibson, Bradford W. APPLICANT: Glibson, Bradford W. APPLICANT: Glibson, Bradford W. APPLICANT: Taylor, Steven W. APPLICANT: Glenn, Cary M. APPLICANT: Warnock, Dale B. TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION TITLE OF INVENTION: DEBRIFEED IN THE MITOCHONDRIAL PROTEOME FILE REFERENCE: 660088.465
| CURRENT APPLICATION NUMBER: US/10/408,765A
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APPLICANT: WOOD, WILLIARM 1.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3530PIC60
CURRENT APPLICATION NUMBER: US/10/219,535
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 1907-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
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PRIOR PILING DATE: 1998-03-27
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Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
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Publication No. US20040044179A1
GENERAL INFORMATION:
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US-10-219-535-42
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	GGTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGGTTTCTGTGAACACAGG	ATAT      aTyr	TGTG	780 ACTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAACCTTCCC-AAAGATCTCCCC 838 	839 ATTATGTTTGANGTCCTGATTCANGANCCTAGCCACTTCCTCAATTATTCTACCATTAAC 898 	899 TACRAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTAAT 958 	959 CACACGIAIGIGCTCAAIGGAACCTICAGCCTIAACCTCACTGIGAAAGCTGCAGCACCA 1018 	1019 GGACCTIGTCCGCCACCGCCACCACCAGACCTTCAAAACCCACCCTTCTTA 1075 	( ) — C	1103 CTGAGTAGGATTCCTGATGAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACC 1162 	1163 ATCACAATTGTAGAGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATG 1222 	1223 CCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATT 1282 	1283 CCCACGGAGGTCTGTACCATTTCTGACCCCACCTGCGAGATCACCCAGAACACACT 1342 	1343 TGCAGCCCTGTGGATGTGGATGTGTGTCTGCTGAGAGAGA	1403 TCTGGGACGTACTGTGACACCTCACCCTGGGGATGACACAAGCCTGGCTCTCAGGAGC 1462 	1463 ACCCTGATTTCTGTTCCTGACAGAGCCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCC 1522 	1523 CTGATCTCCGTTGGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAA 1582

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APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Gedard. Audrey
APPLICANT: Goddard. Audrey
APPLICANT: Goddard. Audrey
APPLICANT: Goddard. Audrey
APPLICANT: Godneski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria L.
APPLICANT: Smith, Victoria L.
APPLICANT: Smith, Victoria L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: ARCHADA, COLOR ENCODING THE SAME
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION ACIDS ENCODING THE SAME
FILE REPERBNCE: 1203-208-29
PRIOR PLILNG DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PRILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063149
PRIOR APPLICATION NUMBER: 60/063149
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Publication No. US20030065147A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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PRIOR APPLICATION NUMBER: 60/069873
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PRIOR PELICATION NUMBER: 60/079910
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US-10-295-027-1041
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Sequence of the sequence of th	Length 2661; Indels 0; Ge CGTCCGTGAGAATTCP CGTCCTGAGAATTCP
ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  GROWTH FACTOR INDUG  463,106  19,272  1,881	); DB 13; ss 0; I TGGTGCCTGC
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. COL OF OF DE 1077. 7 75 CMT/	44 2485 93.4 2683 15 US-10-219-528-41 45 2485 93.4 2683 15 US-10-227-880-41 45 2485 93.4 2683 15 US-10-227-880-41 45 2485 93.4 2683 15 US-10-227-880-41  ALIGNMENTS  SEQUENCE 1, Application US/10463106  Publication No. US20030202938A1  APPLICANT RAMESHWAR, Pranela  TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE JUNERAL INFORMATION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE JUNERING DATE: 2003-06-17  FILE REFERENCE: 267/033 University of Medicine & Dentistry CURRENT FILING DATE: 2003-06-17  PRIOR APPLICATION NUMBER: US 10/039, 272  PRIOR APPLICATION NUMBER: US 60/241, 881  PRIOR APPLICATION NUMBER: US 60/241, 881  NUMBER OF SEQ ID NOS: 2  SOFTWARE: PatentIn version 3.1  LENGTH: 2661  TYPE: DNA  ORGANISM: Homo sapiens  100-673

180 180

61 IGGAAIGICTCTACTATITCCTGGGATTTCTGCTCCTGGCTGCAAAGATTGCCACTTGATG 120

121 CCGCCAAACGATTICATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC 

TGGAATGTCTACTATTTCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG

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126  CSTGACCTGCCAAGGGAGCATTCCCACGGGGTCTGTACCATCATTTCTGACCCCCCTG   120    126  CSTGACCTGCCAAGGGAGCATTCCCACGGGTCTGTGACCTTCTTTCT	1 TTATGETTTCACTTATAAAGTCTTAGGTACTAGTAGGATAGGA
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191 ACAATCAATTAAATGGCTGGTCTTCTGAAGAATGACTGGAATGAAAACTCTACCCAG 240 191 ACAATCAATTAAATGGCTGGTCTTCTGAAGAATGACTGGAAGGACGCTGTGCAGCGG 300 241 TGTGCGAAGCGGGGGAGACATGAGATGAAAATGCTGGAAGGAGGCCGTGCAGGCG 300 241 TGTCGAAGCGGGGGAGACATGAGATGAAAATCCTGGAAGGAGGCCGTGCAGGCG 300 241 TGTCGAAGCGGGGGAGACATGAGATGAAAATCCTGGAAGGAGGCCGTGCAGGCG 300 301 TCCTGACCTGATGACTCAGAGACGCCTCGAAGACATCAAATAAACTTGCGGTGAACCG 300 301 TCCTGACCTGATGACTCAGACTCGAAAAACTCTGGAAGAAGACTCAA 360 302 TCCTGACCTGATGACTCACAAAACTCGGAAGAACTCAAAATAAACTTGCGGTGAACCG 300 303 TATCCCTGACAAAAACTCGAAAAACTCCTGAAAAAAATTAAAATTAACATTGCGGTGAAACAA 360 421 AAATGAGCGCCTGAAAAAAACTCCTGAAAAAAAATTAAAATTAACATTGCGGTGAAACAA 360 421 AAATGAGCGCTGAAAAAAAACTCCTGAAAAAAAAAAAAA	0=0 0=0 4=4 1

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	RESULT 2 US-10-039-272-1 Folication US/10039272 FOURTHALL INFORMATION: GENERAL INFORMATION: APPLICANT: RAMESHWAR, Pranela TITLE OF INVENTION: TITLE OF INVENTION: CURRENT APPLICATION NUMBER: US/10/039,272 CURRENT FILING DATE: 2001-10-20 FRIOR PRIOR APPLICATION NUMBER: US 60/241,881 FRIOR PRIOR SEQ ID NOS: 2 SOFTWARE: Patentin version 3.1 SEQ ID NO 1 LENGTH: 2661 TYPE: DNA	Query Match         100 0%; Score 2661; DB 14; Length 2661;           Best Local Similarity         100 0%; Pred. No. 0;           Matches 2661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;           OY         CGGCACGAGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCTGCTGCTGAGAATTCAGCA 60           Db         1 CGGCACGAGGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCTGCTGCTGAGAATTCAGCA 60           Cb         61 TGGAATGTCTTACTATTTCCTGGGAATTCATGGTGCTGCTGCAGAATTCAGCA 60           Cb         61 TGGAATGTCTTACTATTTCTGGGAATTCATGATTGCTCTGGTGCTGCAGAATTGCACTTGATG           Db         61 TGGAATGTCTTACTATTTCTGGGAATTCATGAATTGCCTTGCTTACATGAGGAGC           Cb         61 TGGAATGTCTTCTACTTTTCTGGTTCTCTGGTTCCTGGCTTACATGAGGAGC           Cb         61 TGGAATGTTTCATGATGTGCTTGGTGGAATGAAAACTCTTGCTTACATGAGGAGC           Cb         61 TGGAATGATTCATGATGTGCTTGCTGGAATGAAAAACTCTGCTTACATGAGGAGC           Cb         61 TGTGGAATGAATTAAATGGTGGTTTCTGATGAAATGAATG

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Sequence 10843, Application US/10198846
; Sequence 10843, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Western Steinmann, Kathleen
APPLICANT: Wang, Youzhen
APPLICANT: WANGYION: UNVELGENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION NUMBER: US/10/198,846
CURRENT FILING DATE: 2001-07-18
; CURRENT FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: PASESEQ for Windows Version 4.0
; SEQ ID NO 10843
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LOCATION: 2950, 2951, 2952
OTHER INFORMATION: n = A,T,C or
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                                                                                                                                     GATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGG
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; Sequence 779, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Wan, Wao
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
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Linsley, Peter S.
Mao, Mao
Roberts, Christopher J.
Van 't Veer, Laura Johanna
Van de Vijver, Marc J.
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; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 66/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR FILING DATE: 2002-05-14
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; ED ID NO 779
; LENGTH: 2669
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-779
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Best Local Similarity
Matches 2591; Conserv
ACGTGGTAACAGATCAGATTCCTGTGTTTTGTGACTATGTTCCAGAAGAACGATCGAAATT
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US-10-172-118-779

US-10-172-118-779

Sequence 779, Application US/10172118

Publication No. US20030224374A1

GENERAL INFORMATION:

APPLICANT: Dai, Hongyue
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breat
CURRENT APPLICATION NUMBER: US/10/172,118

CURRENT APPLICATION NUMBER: 60/380,770
PRIOR APPLICATION DATE: 2002-05-14

PRIOR APPLICATION DOS: 2699

Cancer Patients

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; SEQ ID NO 779
; LENGTH: 2669
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 002510
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-779
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PRIOR APPLICATION NUMBER: US 09/663,733
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PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/334,393
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APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter A
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Masson, Susan R
APPLICANT: Bos Biotechnolo
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APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Matson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
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PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-09
PRIOR FILING DATE: 2002-02-09
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-13
PRIOR FILING DATE: 2002-02
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PRIOR FILING DATE: 2001-04-24
NUMBER OF SEQ ID NOS: 149
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 92
ELENGTH: 2669
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APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN AC
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR TILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: ERRL Program
                                                                                                                                                                                                                                                                      ; Sequence 169, Application Publication No. US20030119; GEMERAL INFORMATION: APPLICANT: Susan Stuart APPLICANT: Jed G. Nuchte; APPLICANT: Jason M. Shoh; APPLICANT: Jason M. Shoh;
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TYPE: DNA
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CAAGCTAACTGAATCCC	TTTCAGCTTTCCATGTAACTG	ACTATTGATT          ACTATTGATT	acttataaagtctta              acttataaagtctta	DAGCCATGTTGTGAAACTGA 	AAATGTO        AAATGTO	CTAAA        CTAAA	CTTGTTTCTGAAGCTC             CTTGTTTCTGAAGCTC	TGTTCTTCCCGGGAAACCAGGAAAAGGATCCG 	CCTGGGAATGTGGTCAGAAGCAAAGGCCTGA 	CTCTTGGTGTACAAAAA                CTCTTGGTGTACAAAAA	GTTCCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTG 	ACGAGCACC	CTTCAATGGGTCT           CTTCAATGGGTCT	CGAGATCACCCAGAACACAGTCTGC: 	TTGCCAAGGGAGCATTCC	CAGATGACAGACGTCCTGATGCCGG	CAGATTAACAGATATGGCCACTTTCAAGCCACCATCA	
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RESULT 10
US-10-219-35-41

| Sequence 41, Application US/10219535
| Publication No. US2004004479A1
| GENERAL INFORMATION:
| APPLICANT: Baker, Kevin P. APPLICANT: Benoyers, Luc APPLICANT: Benoyers, Luc APPLICANT: Gerritsen, Mary APPLICANT: Gerritsen, Mary APPLICANT: Gerritsen, Mary APPLICANT: Gerritsen, Mary APPLICANT: Grinaldi, J. Christopher APPLICANT: Grinaldi, J. Christopher APPLICANT: Stebhan, Jean-Philippe F. APPLICANT: Watanabe, Colin L. APPLICANT: Watanabe, Colin L. APPLICANT: Wood, William I. TITLE OF INVENTION: SCERFED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
| CURRENT PILING DATE: 19330P1C60 | CURRENT PILING DATE: 2002-06-14 |
| PRIOR APPLICATION NUMBER: US/10/219,535 |
| CURRENT APPLICATION NUMBER: 109/119,480 |
| PRIOR APPLICATION NUMBER: 60/059113 |
| PRIOR APPLICATION NUMBER: 60/059113 |
| PRIOR APPLICATION NUMBER: 60/062287 |
| PRIOR APPLICATION NUMBER: 60/06287 |
| PRIOR APPLICATION NUMBER: 60/064103 |
| PRIOR APPLICATION NUMBER: 60/064103 |
| PRIOR APPLICATION NUMBER: 60/069873 |
| PRIOR APPLICATION NUMBER:

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; PRIOR FILING DATE: 1998-03-26; PRIOR APPLICATION INDMER: 60/079728; PRIOR FILING DATE: 1998-03-27; Remaining Prior Application data removed - Se; NUMBER OF SEQ ID NOS: 246; SEQ ID NO 41; SEQ ID NO 41; LENGTH: 2683; TYPE: DNA CORGANISM: Homo Sapien
US-10-219-535-41
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Best Local Similarity 97.8%;
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                                           CATCGAAGAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC
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Sequence 41, Application US/10232230

Publication No. US2004044180A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Gerritsen, Mary

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Girimaldi, J. Christopher

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3530P1C103

CURRENT FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US/10/232,230

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-17
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SEQ ID NO 41
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PRIOR TILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
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WS-10-232-24-41

Sequence 41, Application US/10232224

Publication No. US20030065147A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.

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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 9350PLC111
FILE REFERENCE: 9350PLC111
CURRENT APPLICATION NUMBER: US/10/232,224
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 10/19,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/06973
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/079994
PRIOR APPLICATION NUMBER: 60/079294
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Best Local Similarity
Matches 2576; Conserv
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NUMBER OF SEQ ID NOS: 246
SEQ ID NO 41
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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
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REFERENCE: P3530P1C111
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	TGATGGAACAATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTC	2211	9
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	GTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCACTTCAA	15	Ş
	GAAGAGGCGGGATACTTTCAGCTTTCCATGTAACTGTATGCATAAAGCCAATGTAGTCCA	<u>ب</u> 5	Db
	GAAGAGGCGGGATACTTTCAGCTTTCCATGTAACTGTATGCATAAAGCCAATGTAGTCC	2091	γQ
	TGTCCCGAGAGTAAGGAGAAGCTACTATTGATTAGAGCCCTAACCCAGGTTAACTGCAA 2149	2090	DЪ
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	GAGTTTCTTAAATTTCGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCAITGATGTGAGA 1849	1790	Db
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APPLICANT: Beaker, Kevin P.
APPLICANT: Cedricisen, Wary
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DR FILING DATE: 1998-08-31
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DR FILING DATE: 1998-09-09
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OR PILING DATE: 1999-07-26
OR APPLICATION NUMBER: 60/145698
OR FILING DATE: 1999-07-26
OR APPLICATION NUMBER: 60/146222
OR FILING DATE: 1999-08-03
OR APPLICATION NUMBER: 60/146963
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APPLICATION NUMBER: 60/169445
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APPLICATION 1
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                                              ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGAGACATGAGGTGGA
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PRIOR OR FILING DATE: 1998-09-24

OR APPLICATION NUMBER: 60/101786

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OR APPLICATION NUMBER: 60/10192

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OR APPLICATION NUMBER: 60/106178

OR APPLICATION NUMBER: 60/106248

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OR FILING DATE: 1998-10-29

OR APPLICATION NUMBER: 60/106464

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OR APPLICATION NUMBER: 60/106905

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US-10-20-13-41  US-10-20-13-41  Sequence 41. Application US/0020163  Publication No. US200103663A1:  GENERAL INFORMATION:  APPLICANT: Desmoyers, Luc APPLICANT: Desmoyers, Luc APPLICANT: Geddard, Audrey APPLICANT: Geddard, Audrey APPLICANT: Geddard, Audrey APPLICANT: Geddard, Audrey APPLICANT: Machabe, Colin L.  BEIGN APPLICATION NUMBER: 60/062287  PRIOR APPLICATION NUMBER: 60/062287  PRIOR APPLICATION NUMBER: 60/079294  PRIOR APPLICATION NUMBER: 60/08693  PRIOR APPLICATION NUMBER: 60/08693  PRIOR APPLICATION NUMBER: 60/08693  PRIOR APPLICATION NUMBER: 60/08693  PRIOR APPLICATION NUMBER: 60/086939  PRIOR APPLICATION NUMBER:	Qy 2451 CTGCACATATTTGAAATCAAAATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCA 2510  Db 2510 CTGCACATATTTGAAATC ATATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCA 2568  Qy 2511 TGGCAACTTGATCAGTAAGGATTTCCCCTCTGTTTTGGAACCATATACTATATGT 2570  Db 2569 TGGCAACTTGATCAGTAAGGATTTCACCTCTGTTTTGTAACACCATCTACTATATGT 2628  Qy 2571 TAGACAAGACATTCTTTTTTTTTTCCCTTCCTGAAAAAACACTTAAAACCATCTATATGT 2628  Qy 2571 TAGACAAGACATTTTTTTTTTTTCCCTTCCTGAAAAAAAA
PRIOR FILLING DATE: 1998-08-04 PRIOR APPLICATION NUMBER: 60/095318 PRIOR APPLICATION NUMBER: 60/095318 PRIOR PRIOR DATE: 1998-08-04 PRIOR PRIOR DATE: 1998-08-04 PRIOR PRIOR DATE: 1998-08-01 PRIOR PRIOR PRICATION NUMBER: 60/095916 PRIOR APPLICATION NUMBER: 60/095946 PRIOR APPLICATION NUMBER: 60/095944 PRIOR PRILING DATE: 1998-08-21 PRIOR APPLICATION NUMBER: 60/099594 PRIOR APPLICATION NUMBER: 60/099596 PRIOR APPLICATION NUMBER: 60/099596 PRIOR PRILING DATE: 1998-09-09 PRIOR APPLICATION NUMBER: 60/099803 PRIOR APPLICATION NUMBER: 60/099811 PRIOR APPLICATION NUMBER: 60/099811 PRIOR APPLICATION NUMBER: 60/099812 PRIOR APPLICATION NUMBER: 60/099812 PRIOR APPLICATION NUMBER: 60/099812 PRIOR APPLICATION NUMBER: 60/099812 PRIOR APPLICATION NUMBER: 60/10038 PRIOR PRILING DATE: 1998-09-10 PRIOR APPLICATION NUMBER: 60/10038 PRIOR PRILING DATE: 1998-09-11 PRIOR APPLICATION NUMBER: 60/10038 PRIOR PRILING DATE: 1998-09-15 PRIOR APPLICATION NUMBER: 60/100390 PRIOR APPLICATION NUMBER: 60/100390 PRIOR APPLICATION NUMBER: 60/10044 PRIOR APPLICATION NUMBER: 60/10047 PRIOR APPLICATION NUMBER: 60/10044 PRIOR APPLICATION NUMBER: 60/10178 PRIOR APPLICATION NUMBER: 60/10624 PRIOR PRIOR APPLICATION NUMBER: 60/10624 PRIOR PRIOR APPLICATION NUMBER: 60/10624 PRIOR	PRIOR APPLICATION NUMBER: 60/089905 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/090472 PRIOR FILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090557 PRIOR APPLICATION NUMBER: 60/090691 PRIOR PILING DATE: 1998-06-25 PRIOR PILING DATE: 1998-06-25 PRIOR PILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090695 PRIOR APPLICATION NUMBER: 60/090695 PRIOR APPLICATION NUMBER: 60/091982 PRIOR APPLICATION NUMBER: 60/091982 PRIOR PILING DATE: 1998-07-07 PRIOR PILING DATE: 1998-07-07

PRIOR PELLING DATE: 1999-00-10  PRIOR APPLICATION NUMBER: 60/12549  PRIOR APPLICATION NUMBER: 60/12529  PRIOR APPLICATION NUMBER: 60/12529  PRIOR PELLING DATE: 1999-03-19  PRIOR PELLING DATE: 1999-03-29  PRIOR PELLING DATE: 1999-04-27  PRIOR PELLING DATE: 1999-05-14  PRIOR PELLING DATE: 1999-05-14  PRIOR PELLING DATE: 1999-06-22  PRIOR PELLING DATE: 1999-06-22  PRIOR PELLING DATE: 1999-06-22  PRIOR PELLING DATE: 1999-06-22  PRIOR PELLING DATE: 1999-06-23  PRIOR PELLING DATE: 1999-06-29  PRIOR PELLING DATE: 1999-06-29  PRIOR PELLING DATE: 1999-07-26  PRIOR PELLING DATE: 1999-07-26  PRIOR PELLING DATE: 1999-07-26  PRIOR PELLING DATE: 1999-07-26  PRIOR PELLING DATE: 1999-08-31  PRIOR PELLING DATE	FILING DATE: 1998-11-1 APPLICATION NUMBER: 60 FILING DATE: 1998-11-1 APPLICATION NUMBER: 60 FILING DATE: 1998-12-1 APPLICATION NUMBER: 60 FILING DATE: 1998-12-2 APPLICATION NUMBER: 60 FILING DATE: 1999-01-1 APPLICATION NUMBER: 60
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Sequence 41, Application US/1023038
Publication No. US23030044934A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Godowski, Paul J.
Christopher
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SCERETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C92
CURRENT APPLICATION NUMBER: US/10/230,338
CURRENT APPLICATION NUMBER: 00/05-08-28
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/062287
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079656
PRIOR APPLICATION NUMBER: 60/079728

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; PRIOR FILING DATE
; Remaining Prior #
; NUMBER OF SEQ ID
; SEQ ID NO 41
; SEQ ID NO 41
; LENGTH: 2683
; TYPE: DNA
; ORGANISM: Homo 9
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2628	TGGCAACTTGATCAGTAAGGATTTCACCTCTGTTTGTAACTAAAACCATCTACTATATGT	2569	망
2570	TGGCAACTTGATCAGTAAGGATTTCCCCCTCTGTTTGGAACTAAAACCATTTACTATATGT	2511	8
2568	CTGCACATATTTGAAATC-ATATATTAAGACTTTCCAAAGATGAGGTCCCTGGTTTTTCA	2510	Db
2510	CTGCACATATTTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCA	2451	δ. 20
2509	TATACCAGGCATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTTGTACAGTCG	2450	В
2450	TATACCAGGCATGATGCTGAGTGACACTCTTGTGTATATTTTCCAAATTTTTTGTATAGTCG	2391	Qy
2449	AGTGAAGGAATGATATTCATATATTCATTTATTCCATGGACATTTAGTTAG	2390	DЬ
2390	AGTGAAGGAATGATATTCATATATTCATTTATTCCATGGACATTTAGTTAG	2331	γQ
2389	AAAATACTACTCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTG	2330	DЪ
2330	AAAATACTACTCTCATAAATGGGTGGGAGTATTTTTGGTGACAACCTACTTTGCTTGGCTG	2271	8
2329	TGATGGAACAATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAA	2270	뫄
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2269	GTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCACTTCAATACACACTCATGAACTCC	2210	뫄
2210	GTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCACTTCAATACACACTCATGAACTCC	2151	Ş
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2150	GAAGAGGCGGGATACTTTCCAGCTTTCCATGTAACTGTATGCATAAAGCCAATGTAGTCCA	2091	Q.
2149	TGTCCCGAGAGTAAGGAAGAAGCTACTATTGATTAGAGCCTAACCCAGGTTAACTGCAA	2090	Db
2090	TGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTTAACTGCAA	2031	8
2089	TICATTATETTTATGTTTCACTTATAAGTCTTAGGTAACTAGTAGGATAGAAACACTG	2030	DЪ